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OM protein - protein search, using sw model

Run on: August 26, 2002, 15:49:03 ; Search time 29.93 Seconds

(Without alignments)
111.334 Million cell updates/sec

Title: US-09-813-345-2

Perfect score: 150

Sequence: 1 THRRLAGLSRSGMVKSNFVPTNVSRAF 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_032802:*

- 1: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
- 2: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
- 3: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
- 4: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
- 5: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
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- 7: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*
- 8: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:*
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- 10: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:*
- 11: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*
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- 14: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*
- 15: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:*
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- 17: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:*
- 18: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*
- 19: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
- 20: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
- 21: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	150	100.0	30	22	AAE09806
2	135.5	90.3	29	22	AAE09805
3	135.5	90.3	36	14	AAE09805
4	135.5	90.3	36	14	AAE09805
5	135.5	90.3	36	14	AAE09805
6	135.5	90.3	36	14	AAE09805
7	135.5	90.3	36	14	AAE09805
8	135.5	90.3	36	14	AAE09805
9	135.5	90.3	36	14	AAE09805
10	135.5	90.3	36	14	AAE09805
11	135.5	90.3	36	14	AAE09805

12	135.5	90.3	38	7	AAE09805	Sequence of calcit
13	135.5	90.3	38	22	AAE09805	Calcitonin gene r
14	135.5	90.3	39	7	AAE09805	Sequence of calcit
15	135.5	90.3	72	7	AAE09805	Sequence of calcit
16	132.5	88.3	37	11	AAE09805	Calcitonin gene re
17	132.5	88.3	37	11	AAE09805	Calcitonin gene re
18	131.5	87.7	37	11	AAE09805	Calcitonin gene re
19	131.5	87.7	37	11	AAE09805	Calcitonin gene re
20	128.5	85.7	29	14	AAE09805	9-37 peptide B. S
21	128.5	85.7	30	15	AAE09805	(8-37)-CGRP. Homo
22	128.5	85.7	30	22	AAE09805	Calcitonin gene r
23	128.5	85.7	35	21	AAE09805	pep 15 used in nuc
24	128.5	85.7	35	21	AAE09805	Peptide ligand pep
25	128.5	85.7	35	22	AAE09805	Nucleic acid trans
26	128.5	85.7	35	22	AAE09805	Nucleic acid trans
27	128.5	85.7	36	14	AAE09805	Desalanyl [Asu2,7]
28	128.5	85.7	36	14	AAE09805	Desalanyl [Asu2,7]
29	128.5	85.7	37	5	AAE09805	Calcitonin gene re
30	128.5	85.7	37	6	AAE09805	Sequence of human
31	128.5	85.7	37	6	AAE09805	Precursor of human
32	128.5	85.7	37	11	AAE09805	Calcitonin gene re
33	128.5	85.7	37	11	AAE09805	Calcitonin gene re
34	128.5	85.7	37	14	AAE09805	Calcitonin gene re
35	128.5	85.7	37	14	AAE09805	Human alpha-CGRP
36	128.5	85.7	37	16	AAE09805	Human alpha-CGRP
37	128.5	85.7	37	18	AAE09805	Human calcitonin g
38	128.5	85.7	37	18	AAE09805	Human calcitonin g
39	128.5	85.7	37	19	AAE09805	Alpha form of calc
40	128.5	85.7	37	20	AAE09805	Alpha-Calcitonin-g
41	128.5	85.7	37	20	AAE09805	Calcitonin gene re
42	128.5	85.7	37	22	AAE09805	Human calcitonin g
43	128.5	85.7	37	22	AAE09805	Calcitonin gene r
44	128.5	85.7	37	22	AAE09805	Calcitonin gene r
45	128.5	85.7	38	21	AAE09805	Human alpha-calcit

ALIGNMENTS

RESULT 1	
AAE09806	AAE09806 standard; peptide: 30 AA.
XX	
AC	AAE09806;
XX	
DT	29-NOV-2001 (first entry)
XX	
DE	Alpha-calcitonin gene related peptide (alpha-CGRP).
XX	
KW	Vasoactive peptide; calcitonin gene related peptide; CGRP;
KW	CGRP-receptor identification.
XX	
OS	Unidentified.
XX	
PN	US6268474-B1.
XX	
PD	31-JUL-2001.
XX	
PF	30-APR-1998; 98US-0070504.
XX	
PR	30-APR-1998; 98US-0070504.
XX	
PA	(UYCR-) UNIV CREIGHTON.
XX	
PI	Smith DD, Saha S, Abel PW;
XX	
DR	WPI: 2001-564216/63.
XX	
PT	Vasoactive peptides useful for inhibiting calcitonin gene related
PT	peptide receptor activity -
XX	
PS	Claim 2; Column 2; 24pp; English.
XX	

CC The invention relates to antagonists of the vasoactive peptide
 CC calcitonin gene related peptide (CGRP) and other members of the
 CC CGRP superfamily. The invention also relates to amino the terminal
 CC modifications of peptides to improve their ability to bind to a
 CC member of the CGRP-receptor super-family. CGRP antagonists are
 CC used for inhibiting CGRP activity which can be used in vitro e.g.
 CC in assays to identify and/or isolate CGRP receptors or with intact
 CC cells either in vitro or in vivo to inhibit the effect of CGRP
 CC binding to its receptor. The present sequence is alpha-CGRP peptide
 CC (8-37).
 CC
 XX
 SQ Sequence 30 AA;

Query Match 100.0%; Score 150; DB 22; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1.3e-16;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 THRLAGLSRSGMWKSNFVPTNVGSKAF 30
 |||||
 DB 1 thrlaglsrsgmwksnfvptnvyskaf 30

RESULT 2
 ID AAE09805 standard; peptide; 29 AA.
 AC AAE09805;
 XX
 XX 29-NOV-2001 (first entry)
 DE Beta-calcitonin gene related peptide (beta-CGRP).
 KW Vasoactive peptide; calcitonin gene related peptide; CGRP;
 KW CGRP-receptor identification.
 OS Unidentified.
 OS
 XX US6268474-B1.
 PN 31-JUL-2001.
 PD 30-APR-1998; 98US-0070504.
 PF 30-APR-1998; 98US-0070504.
 XX
 PR 30-APR-1998; 98US-0070504.
 XX
 PA (UYCR-) UNIV CREIGHTON.
 PI Smith DD, Saha S, Abel PW;
 DR WPI; 2001-564216/63.
 XX
 PT Vasoactive peptides useful for inhibiting calcitonin gene related
 PT peptide receptor activity -
 XX
 PS Claim 2; Column 2; 24pp; English.
 XX
 CC The invention relates to antagonists of the vasoactive peptide
 CC calcitonin gene related peptide (CGRP) and other members of the
 CC CGRP superfamily. The invention also relates to amino the terminal
 CC modifications of peptides to improve their ability to bind to a
 CC member of the CGRP-receptor super-family. CGRP antagonists are
 CC used for inhibiting CGRP activity which can be used in vitro e.g.
 CC in assays to identify and/or isolate CGRP receptors or with intact
 CC cells either in vitro or in vivo to inhibit the effect of CGRP
 CC binding to its receptor. The present sequence is beta-CGRP peptide
 CC (8-37).
 CC
 XX
 SQ Sequence 29 AA;

Query Match 90.3%; Score 135.5; DB 22; Length 29;
 Best Local Similarity 96.7%; Pred. No. 2.5e-14;

Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGMWKSNFVPTNVGSKAF 30
 |||||
 DB 1 thrlaglsrsgmwksnf-vptnvyskaf 29

RESULT 3
 ID AAR42019 standard; peptide; 36 AA.
 AC AAR42019;
 XX
 XX 08-NOV-1993 (first entry)
 DE Desalanyl-desamino human beta-CGRP.
 KW Human; calcitonin gene related peptide; CGRP; blood pressure;
 KW regulation; hypertension; surgery; hypotensive anaesthesia;
 KW cerebrovascular disorders.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note="Desamino-Cys"
 FT Disulfide-bond 1..6
 XX
 PN WO9311787-A.
 PD 24-JUN-1993.
 PF 08-DEC-1992; 92WO-JP01600.
 XX
 PR 12-DEC-1991; 91JP-0329065.
 PR 02-DEC-1992; 92JP-0323445.
 XX
 PA (ASAH) ASAMI KASEI KOGYO KK.
 PI Matsumoto K, Shirai T, Takeda S;
 DR WPI; 1993-213820/26.
 XX
 PT New hypotensive agent contg. calcitonin gene related peptide -
 PT useful in regulating blood pressure during surgery
 XX
 PS Claim 3; Page 3 and 20; 32pp; Japanese.
 XX
 CC The sequences given in AAR42018-37 represent derivatives of the human
 CC alpha and beta calcitonin gene related peptides (CGRP). These
 CC peptides may be used in a blood pressure regulating agent. This
 CC agent may be used in the treatment of hypertension during surgery,
 CC for the regulation of blood pressure, during hypotensive anaesthesia
 CC and in the treatment of cerebrovascular disorders. The agent is fast
 CC acting and gives high controllability of blood pressure. See also
 CC AAR38662-67.
 CC
 XX
 SQ Sequence 36 AA;

Query Match 90.3%; Score 135.5; DB 14; Length 36;
 Best Local Similarity 96.7%; Pred. No. 3.2e-14;
 Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGMWKSNFVPTNVGSKAF 30
 |||||
 DB 8 thrlaglsrsgmwksnf-vptnvyskaf 36

RESULT 4
 ID AAR42021 standard; peptide; 36 AA.
 XX

```

AC  AAR42021;
XX
XX  08-NOV-1993 (first entry)
XX
DE  Desalanyl [Asu2,7] human beta-CGRP.
XX
XX  Human; calcitonin gene related peptide; CGRP; blood pressure;
KW  regulation; hypertension; surgery; hypotensive anaesthesia;
XX  cerebrovascular disorders.
XX
OS  Synthetic.
XX
FH  Key Location/Qualifiers
FT  Modified-site 1
FT  /note="Desamino-Cys, N-terminally modified by Asu
FT  at position 6"
FT  Misc-difference 6
FT  /label=OTHER
FT  /note="Asu, linked to the N-terminal of Cys1"
XX
XX  WO9311787-A.
XX
XX  24-JUN-1993.
XX
XX  08-DEC-1992; 92WO-JP01600.
XX
XX  12-DEC-1991; 91JP-0329065.
XX  02-DEC-1992; 92JP-0323445.
XX
XX  (ASAH ) ASAMI KASEI KOGYO KK.
XX
XX  Matsumoto K, Shirai T, Takeda S;
XX
XX  WPI; 1993-213820/26.
XX
XX  New hypotensive agent contg. calcitonin gene related peptide -
FT  useful in regulating blood pressure during surgery
XX
XX  Claim 3; Page 3 and 20; 32pp; Japanese.
XX
XX  The sequences given in AAR42018-37 represent derivatives of the human
CC  alpha and beta calcitonin gene related peptides (CGRP). These
CC  peptides may be used in a blood pressure regulating agent. This
CC  agent may be used in the treatment of hypertension during surgery,
CC  for the regulation of blood pressure, during hypotensive anaesthesia
CC  and in the treatment of cerebrovascular disorders. The agent is fast
CC  acting and gives high controllability of blood pressure. See also
CC  AAR38662-67.
XX
XX
XX  Sequence 36 AA;
SQ

```

Query Match 90.3%; Score 135.5; DB 14; Length 36;
 Best Local Similarity 96.7%; Pred. No. 3.2e-14;
 Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

OY  1 THRAGLISRSRGWVNFVPTNVGSKAF 30
    |||||
DB  8 thrlagllstrsgmwksnf-vptnvgska 36

```

RESULT 5
 AAP60352
 ID AAP60352 standard; Peptide; 37 AA.
 AC AAP60352;
 DT 08-AUG-1991 (first entry)
 DE Sequence of calcitonin-gene-related peptide (CGRP) (IV).
 KW Vasodilatory; hypocalcaemic; hypotensive; myocardial contractility.
 XX

```

OS  Homo sapiens.
XX
XX  EP188400-A.
XX
XX  23-JUL-1986.
XX
XX  10-JAN-1986; 86EP-0810007.
XX
XX  16-JAN-1985; 85CH-0000188.
XX
XX  (CIBA ) CIBA GEIGY AG.
XX
XX  Jansz HS, Lips CJM, Steenbergh PH, Rink H;
XX
XX  WPI; 1986-191184/30.
XX  N-PSDB; AAN60266, AAN60267, AAN60268.
XX
XX  New calcitonin gene related peptide(s) and peptide amide(s) -
PT  with vasodilatory, hypotensive, gastric secretion inhibiting, CNS
PT  and hypocalcaemic activity
XX
XX  Claim 1; Page 85 and 33; 96pp; German.
XX
XX  The inventors claim calcitonin-gene-related peptides (CGRP) contg.
CC  the aa sequence in AAP60352 as part of a larger peptide with up to 90
CC  aa residues, or as the sole aa sequence, their derivs. with amidated
CC  terminal carboxyl gp. and/ or acylated terminal amino gp., and their
CC  salts. The cysteine residues can form intra- or inter-molecular
CC  disulphide bridges. Also claimed are DNA sequences (AAN60266, AAN60268)
CC  as a partial sequence of a larger sequence with up to 290
CC  deoxyneucleotides in a single strand.
XX
XX
XX  Sequence 37 AA;
SQ

```

Query Match 90.3%; Score 135.5; DB 7; Length 37;
 Best Local Similarity 96.7%; Pred. No. 3.3e-14;
 Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

OY  1 THRAGLISRSRGWVNFVPTNVGSKAF 30
    |||||
DB  9 thrlagllstrsgmwksnf-vptnvgska 37

```

RESULT 6
 AAR04519
 ID AAR04519 standard; peptide; 37 AA.
 AC AAR04519;
 DT 18-SEP-1990 (first entry)
 DE Calcitonin gene related peptide analogue.
 KW Calcitonin; cerebral blood supply deficiencies;
 KW subarachnoid haemorrhage; stroke; migraine.
 OS Synthetic.
 PN EP367463-A.
 PD 09-MAY-1990.
 PF 20-OCT-1989; 89EP-0310859.
 PR 20-OCT-1988; 88GB-0000877.
 XX (CELL-) CELLTech LTD.
 XX Paton MAM, Beeley NRA, Rose CC;
 XX WPI; 1990-141386/19.
 XX

PT New analogues of calcitonin gene related peptide -
 PT selectively increase blood flow in the carotid arteries, useful
 PT for treating cerebral blood supply deficiencies.

PS Claim 7; Page 11; 19pp; English.

CC Useful in treating cerebral blood supply deficiencies, such as
 CC cerebral stroke, subarachnoid haemorrhage or migraine. The
 CC compounds may also be useful in treating cardiac disorders and
 CC hypertension.

XX Sequence 37 AA;

Query Match 90.3%; Score 135.5; DB 11; Length 37;
 Best Local Similarity 96.7%; Pred. No. 3.3e-14;
 Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGWVKNFVPTNGSKAF 30
 |||||
 Db 9 thrlaglsrsgwmvknf-vptnyskaf 37

RESULT 7

AA38663 standard; peptide; 37 AA.

AA38663;

08-NOV-1993 (first entry)

Human beta-CGRP.

Human; calcitonin gene related peptide; CGRP; blood pressure;
 regulation; hypertension; surgery; hypotensive anaesthesia;
 cerebrovascular disorders.

Homo sapiens.

Key Location/Qualifiers

Disulfide-bond 2..7

WO9311787-A.

24-JUN-1993.

08-DEC-1992; 92WO-JP01600.

12-DEC-1991; 91JP-0329065.

02-DEC-1992; 92JP-0323445.

(ASAH) ASAH KASEI KOGYO KK.

Matsumoto K, Shirai T, Takeda S;

WPI; 1993-213820/26.

New hypotensive agent conty. calcitonin gene related peptide -
 useful in regulating blood pressure during surgery

Claim 2; Page 3; 32pp; Japanese.

This sequence represents the human beta calcitonin gene related
 peptide (CGRP). This peptide, or derivatives of it, may be used in
 a blood pressure regulating agent. This agent may be used in the
 treatment of hypertension during surgery, for the regulation of
 blood pressure, during hypotensive anaesthesia and in the treatment
 of cerebrovascular disorders. The agent is fast acting and gives
 high controllability of blood pressure. See also AAR4018-37.

Sequence 37 AA;

Query Match 90.3%; Score 135.5; DB 14; Length 37;
 Best Local Similarity 96.7%; Pred. No. 3.3e-14;
 Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGWVKNFVPTNGSKAF 30
 |||||
 Db 9 thrlaglsrsgwmvknf-vptnyskaf 37

RESULT 8

AAW31915 standard; peptide; 37 AA.

AAW31915;

02-APR-1998 (first entry)

Beta form of calcitonin gene-related peptide.

Calcitonin gene-related peptide; beta-CGRP; cardiovascular system;
 progesterin; L-arginine donor; nitric oxide donor; preeclampsia; eclampsia;
 pregnancy; preterm labour; NG-nitro-L-arginine methyl ester; L-NAME;
 hypertension.

Homo sapiens.

Key Location/Qualifiers

Disulfide-bond 2..7

Modified-site 37 /note="C-terminal amide"

WO9734922-A1.

25-SEP-1997.

18-MAR-1997; 97WO-US04310.

19-MAR-1996; 96US-0619841.

(TEXA) UNIV TEXAS SYSTEM.

Wimalawansa SJ, Yallampalli C;

WPI; 1997-480159/44.

Composition for treating (pre)eclampsia of pregnancy or preterm
 labour - comprises calcitonin gene-related peptide or analogue and a
 progesterin and/or nitric oxide donor

Claim 11; Page 22; 38pp; English.

This sequence represents the beta-form of the human calcitonin
 gene-related peptide (beta-CGRP). The alpha- and beta-CGRP's differ in
 structure by only three amino acids, and each possesses equal biological
 activity in the cardiovascular system. This sequence, and alpha-CGRP can
 be used in the composition of the invention which comprises a
 therapeutically effective amount of CGRP or CGRP analogue; and (a) a
 progestin; and/or (b) L-arginine or nitric oxide donor. The composition
 is specifically used to treat preeclampsia and eclampsia of pregnancy, or
 preterm labour in a pregnant female mammal. CGRP may also be used to
 remedy NG-nitro-L-arginine methyl ester (L-NAME) induced hypertension.
 CC The amino acid residues of the potential cleavage sites have been
 CC modified to inhibit biodegradation of CGRP in vivo (no specific details
 given).

Sequence 37 AA;

Query Match 90.3%; Score 135.5; DB 18; Length 37;
 Best Local Similarity 96.7%; Pred. No. 3.3e-14;
 Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGWVKNFVPTNGSKAF 30

Db 9 thrlagllsrsgmwnf-vptnvgskaf 37

RESULT 9
AAV39870
ID AAV39870 standard; peptide: 37 AA.

AC AAV39870;

DT 03-DEC-1999 (first entry)

DE Calcitonin gene related peptide beta form.

KM Calcitonin gene related peptide; CGRP; beta form; human; angioplasty;
KM pathological vasospasm; ischaemia; impotence; vasoconstrictor peptide;
KM blood vessel reocclusion; stent insertion; vascular graft; renal failure;
therapy.

OS Homo sapiens.

PN US5958877-A.

PD 28-SEP-1999.

PF 18-MAY-1995; 95US-0446929.

PR 18-MAY-1995; 95US-0446929.

PA (WIMA/) WIMALAWANSA S J.

PI Wimalawansa SJ;

DR WPI: 1999-561061/47.

PT Counteracting pathological vasospasms or ischaemia in target arteries

PS and treatment of impotence -

CC Disclosure; Column 9-10; 9pp; English.

CC This sequence represents the beta form of human calcitonin gene-related
CC peptide (CGRP). The invention relates to a method for counteracting
CC pathological vasospasms or ischaemia in target arteries (coronary,
CC carotid, and renal arteries) comprising administration of CGRP. The
CC method is useful for the treatment of impotence and for prevention of
CC vasospasms induced by vasoconstrictor peptides, particularly during
CC angioplasty or to prevent reocclusion of blood vessels during and/or
CC after either angioplasty, stent insertion, or the implantation of a
CC vascular graft. The method can also be used to treat renal failure. The
CC effects of CGRP are limited to local vascular area, no systemic effects
CC are induced, making it safe and effective. The method is less invasive
CC for treatment of reocclusion compared to intracoronary stents (prior
CC art).

CC Sequence 37 AA;

CC SQ

Query Match 90.3%; Score 135.5; DB 20; Length 37;
Best Local Similarity 96.7%; Pred. No. 3.3e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLLSRSGMWNFVPTNNGSKAF 30
Db 9 thrlagllsrsgmwnf-vptnvgskaf 37

RESULT 10

ID AAB91062 standard; Peptide: 37 AA.

AC AAB91062;

DT 22-JUN-2001 (first entry)

XX Calcitonins gene related peptide (CGRP) SEQ ID NO:236.

KM protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.
OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

DR WPI: 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 267; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (II) and a
CC reactive group (III) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

CC Sequence 37 AA;

CC SQ

Query Match 90.3%; Score 135.5; DB 22; Length 37;
Best Local Similarity 96.7%; Pred. No. 3.3e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLLSRSGMWNFVPTNNGSKAF 30
Db 9 thrlagllsrsgmwnf-vptnvgskaf 37

RESULT 11

ID AAE09807 standard; peptide: 37 AA.

AC AAE09807;

DT 29-NOV-2001 (first entry)

DE Human beta-calcitonin gene related peptide (beta-CGRP).

KM Human; vasoactive peptide; calcitonin gene related peptide; CGRP;

CC The invention relates to antagonists of the vasoactive peptide
CC calcitonin gene related peptide (CGRP) and other members of the
CC CGRP superfamily. The invention also relates to amino terminal
CC modifications of peptides to improve their ability to bind to a
CC member of the CGRP-receptor super-family. CGRP antagonists are
CC used for inhibiting CGRP activity which can be used *in vitro* e.g.
CC in assays to identify and/or isolate CGRP receptors or with intact
CC cells either *in vitro* or *in vivo* to inhibit the effect of CGRP
CC binding to its receptor. The present sequence is human beta-CGRP
CC peptide.
XX
XX
XX Sequence 37 AA;
XX

Qy	1	THR	LAG	L	S	R	S	G	M	V	K	S	N	F	V	P	T	N	V	G	S	K	A	F	30
Db	9	thr	lag	l	s	r	s	g	m	v	k	s	n	f	v	p	t	n	v	g	s	k	a	f	37

ID AAP60353 standard; Peptide; 38 AA.

DT 08-AUG-1991 (first entry)

Vasodilatory; hypocalcaemic; hypotensive; myocardial contractility.

EH	key	Location/Qualifiers
ET	new1 fido-board	2 7

AA
PN
FP188400-A

PF 10-JAN-1986; 86EP-0810007.

PR 16-JAN-1985; 85CH-0000188.

	Query Match	Similarity	90-3%	Score	135.5;	D8	7;	Length	38;	
	Best Local	Similarity	96.7%;	Pred.	No.	3,4e-14;				
	Matches	29;	Conservative	0;	Mismatches	0;	Indels	1;	Gaps	1;
QY	1	THRLAGLLSRSGMKVKSNEFVPNTNGSKAF	30							
Db	9	tnrlagllsrsgmksnfl-vplnvgskaif	37							

RESULT 13
AAB91075
ID AAB91075 standard; Peptide; 38 AA.

DT 22-JUN-2001 (first entry)
 XX

DE
XY
Calcitonins gene related peptide (CGRP) SEQ ID NO:249.

kw blood component: succinimidyl: maleimido group: amine:
nm Protection; enalaprilic peptide; peptidase; conjugation;
Protection; enalaprilic peptide; peptidase; conjugation;

[illegible]

Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR	17-MAY-1999;	99US-0134406.
DD	18 MAY 1999	0000 0153406

PR 15-OCT-1999; 99US-0159783.

PA (CONJ-) CONJUCHEM INC
XX

XX
F1 BRADON DP, EZLIN AM, MILNER PG, HOLMES DL, TINDAUBEAU K,
XX

DR WFL; 2001-112039/12
XX

PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 272; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)

CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide) and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

Sequence 38 AA:

Query Match 90.3%; Score 135.5; DB 22; Length 38;
 Best Local Similarity 96.7%; Pred. No. 3,4e-14;
 Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGMWKSNFVPTNVGSKAF 30
 |||||
 Db 10 thrlagllsrsgmwksnf-vptnvgskaf 38

RESULT 14

AAP60354 ID AAP60354 standard; Peptide: 39 AA.

AC AAP60354;

DT 08-AUG-1991 (first entry)

XX Sequence of calcitonin-gene-related peptide (CGRP) (XVII).

XX Vasodilatory; hypocalcaemic; hypotensive; myocardial contractility.

XX Homo sapiens.

XX EPI88400-A.

XX 23-JUL-1986.

XX 10-JAN-1986; 86EP-0810007.

XX 16-JAN-1985; 85CH-0000188.

XX (CIBA) CIBA GEIGY AG.

XX Jansz HS, Lips CJM, Steenbergh PH, Rink H;

XX WPI; 1986-191184/30.

XX N-PSDB; AAN60271.

XX New calcitonin gene related peptide(s) and peptide amide(s) -
 PT with vasodilatory, hypotensive, gastric secretion inhibiting, CNS
 PT and hypocalcaemic activity

XX Claim 1; Page 85 and 33; 96pp; German.

XX The inventors claim calcitonin-gene-related peptides (CGRP) contg.
 CC the aa sequence in AAP60352 as part of a larger peptide with up to 90
 CC aa residues, or as the sole aa sequence, their derivs. with amidated
 CC terminal carboxyl gp. and/ or acylated terminal amino gp., and their
 CC salts. The cysteine residues can form intra- or inter-molecular
 CC disulphide bridges. Also claimed are DNA sequences (AAN60266, AAN60268)
 CC as a partial sequence of a larger sequence with up to 290
 CC deoxynucleotides in a single strand.

SO Sequence 39 AA:

Query Match 90.3%; Score 135.5; DB 7; Length 39;
 Best Local Similarity 96.7%; Pred. No. 3,5e-14;
 Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGMWKSNFVPTNVGSKAF 30
 |||||
 Db 10 thrlagllsrsgmwksnf-vptnvgskaf 38

RESULT 15

AAP60341 ID AAP60341 standard; peptide: 72 AA.

AC AAP60341;

DT 08-AUG-1991 (first entry)

XX Sequence of calcitonin-gene-related peptide (CGRP) (II).

XX Vasodilatory; hypocalcaemic; hypotensive; myocardial contractility.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT Region 27..63 /note="Claimed = AAP60352"

XX EPI88400-A.

XX 23-JUL-1986.

XX 10-JAN-1986; 86EP-0810007.

XX 16-JAN-1985; 85CH-0000188.

XX (CIBA) CIBA GEIGY AG.

XX Jansz HS, Lips CJM, Steenbergh PH, Rink H;

XX WPI; 1986-191184/30.

XX New calcitonin gene related peptide(s) and peptide amide(s) -
 PT with vasodilatory, hypotensive, gastric secretion inhibiting, CNS
 PT and hypocalcaemic activity

XX Disclosure: Page 2; 96pp; German.

XX The inventors claim calcitonin-gene-related peptides (CGRP) contg.
 CC the aa sequence in AAP60352 as part of a larger peptide with up to 90
 CC aa residues, or as the sole aa sequence, their derivs. with amidated
 CC terminal carboxyl gp. and/ or acylated terminal amino gp., and their
 CC salts. The cysteine residues can form intra- or inter-molecular
 CC disulphide bridges. Also claimed are DNA sequences (AAN60266, AAN60268)
 CC as a partial sequence of a larger sequence with up to 290
 CC deoxynucleotides in a single strand.

SO Sequence 72 AA:

Query Match 90.3%; Score 135.5; DB 7; Length 72;
 Best Local Similarity 96.7%; Pred. No. 7,3e-14;
 Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGMWKSNFVPTNVGSKAF 30
 |||||
 Db 35 thrlagllsrsgmwksnf-vptnvgskaf 63

Search completed: August 26, 2002, 15:51:55

Job time: 172 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 26, 2002, 15:50:28 ; Search time 14.83 Seconds

(without alignments)
194.382 Million cell updates/sec

Title: US-09-813-345-2

Perfect score: 150
Sequence: 1 THRLAGLLSRSGMWKSNFVPTNVGSKAF 30Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	135.5	90.3	72	2	I37232
2	135.5	90.3	127	2	A25864
3	128.5	85.7	128	1	TCRHR
4	127.5	85.0	37	2	JH0709
5	123.5	82.3	128	1	TCRTR
6	122.5	81.7	134	2	A44173
7	118.5	79.0	128	2	B44173
8	110.5	73.7	125	1	TCCHRP
9	52	34.7	449	2	A48939
10	51	34.0	474	1	I40059
11	51	34.0	474	2	A13349
12	50.5	33.7	89	2	A13542
13	50.5	33.7	135	2	A56855
14	49.5	33.0	261	2	T04301
15	49	32.7	157	2	A24434
16	49	32.7	516	2	US0083
17	49	32.7	516	2	S33164
18	49	32.7	1029	2	T30852
19	48.5	32.3	93	1	TCRTR
20	48.5	32.3	93	1	C33542
21	48	32.0	428	1	SYCR
22	48	32.0	428	2	D90629
23	48	32.0	428	2	D85480
24	48	32.0	429	2	D70784
25	48	32.0	533	2	F70171
26	48	32.0	875	2	T17382
27	48	32.0	1608	1	MMTMGM
28	48	32.0	2021	1	A97859
29	47.5	31.7	89	2	S22344

30	47.5	31.7	385	2	C97277	glycosyltransferas
31	47	31.3	428	2	AE0502	threonine synthase
32	47	31.3	711	2	F65201	phosphoenolpyruvat
33	47	31.3	711	2	D91238	PEP-protein phosph
34	47	31.3	711	2	H86085	PEP-protein phosph
35	47	31.3	995	2	C83203	probable serine pr
36	46	30.7	68	2	G81063	hypothetical prote
37	46	30.7	167	2	E87476	conserved hypothet
38	46	30.7	230	2	G81960	hypothetical inner
39	46	30.7	230	2	B81017	conserved hypothet
40	46	30.7	258	2	I40374	N-acetylglutamate
41	46	30.7	232	2	E90180	conserved hypothet
42	46	30.7	400	2	T19517	hypothetical prote
43	46	30.7	434	2	S62813	MG181 homolog G99
44	46	30.7	849	2	T04242	abdominal segment
45	46	30.7	870	2	AE0208	probable outer mem

ALIGNMENTS

RESULT 1

I37232

calcitonin gene-related peptide 2 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 16-Jul-1999

C:Accession: I37232

R:Steenbergh, P.H.; Hoppenner, J.W.; Zandberg, J.; Lips, C.J.; Jansz, H.S.

FEBS Lett. 183, 403-407, 1985

A:Title: A second human calcitonin/CGRP gene.

A:Reference number: I37232; MUID:85180007

A:Accession: I37232

A:Status: preliminary; translated from GB/EMBL/DDAJ

A:Molecule type: mRNA

A:Residues: 1-72 <RES>

A:Cross-references: EMBL:X02404; NID:g29933; PIDN:CA26249.1; PID:g825642

C:Superfamily: calcitonin

Query Match 90.3%; Score 135.5; DB 2; Length 72;

Best Local Similarity 96.7%; Pred. No. 6.2e-13;

Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 THRLAGLLSRSGMWKSNFVPTNVGSKAF 30

DB 35 THRLAGLLSRSGMWKSNF-VPTNVGSKAF 63

RESULT 2

calcitonin gene-related peptide beta precursor - human

N:Alternate names: calcitonin gene-related peptide II

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 29-Aug-1997

C:Accession: A25864; JH0620; E26142; A34565

R:Steenbergh, P.H.; Hoepfner, J.W.M.; Zandberg, J.; Visser, A.; Lips, C.J.M.; Jansz,

FEBS Lett. 209, 97-103, 1986

A:Title: Structure and expression of the human calcitonin/CGRP genes.

A:Reference number: A25864; MUID:87105923

A:Accession: A25864

A:Molecule type: DNA

A:Residues: 1-127 <STP>

R:Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Matsuo, H.; Eto, T.

Biochem. Biophys. Res. Commun. 185, 134-141, 1992

A:Title: Isolation and characterization of peptides which act on rat platelets, from

A:Reference number: JH0618; MUID:92287083

A:Accession: JH0620

A:Molecule type: protein

A:Residues: 82, 'X', 84-87, 'X', 89-104 <KIT>

A:Experimental source: pheochromocytoma

R:Pettermann, J.B.; Born, W.; Chang, J.Y.; Fischer, J.A.

J. Biol. Chem. 262, 542-545, 1987

A:Title: Identification in the human central nervous system, pituitary, and thyroid o

A:Reference number: A92637; MUID:87109142
 A:Accession: B26142
 A:Molecule type: protein
 A:Residues: 82,'X','84-87','X','89-91','X','93-98','X','100-105','X','107-109 <P>
 Biochem. Biophys. Res. Commun. 167, 993-1000, 1990
 A:Title: Isolation, purification and characterization of beta-hCGRP from human spinal cord
 A:Reference number: A34565; MUID:90211348
 A:Accession: A34565
 A:Molecule type: protein
 A:Residues: 82-86;104-117 <MIM>
 C:Comment: Calcitonin gene-related peptide II peptide is a potent vasorelaxant.
 C:Genetics:
 A:Gene: GDB:CALCB; CALC2
 A:Cross-references: GDB:120572; OMIM:114160
 A:Map position: 11p15.2-11p15.1
 C:Superfamily: calcitonin
 C:Keywords: amidated carboxyl end; neuropeptide
 F:82-118/Product: calcitonin gene-related peptide beta #status experimental <MAT>
 F:83-88/Disulfide bonds: #status experimental
 F:118/Modified site: amidated carboxyl end (Phe) (amide in mature form from following g

Query Match 90.3%; Score 135.5; DB 2; Length 127;
 Best Local Similarity 96.7%; Pred. No. 1,2e-12;
 Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRAGLLSRSGGWKSNFVPTNYSKAF 30
 |||||
 DB 90 THRAGLLSRSGGWKSNF-VPTNYSKAF 118

RESULT 3
 TCHDR
 calcitonin gene-related peptide alpha precursor [validated] - human
 N:Alternate names: calcitonin gene-related peptide I; CGRP-I
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1987 #sequence_revision 02-Jul-1996 #text_change 08-Dec-2000
 C:Accession: S07644; A22943; B22716; I5536; J00005; S10813; A26142; JH0619; I52204; I84
 R:Broad, P.M.; Symes, A.J.; Thakker, R.V.; Craig, R.K.
 Nucleic Acids Res. 17, 6999-7011, 1989
 A:Title: Structure and methylation of the human calcitonin/alpha-CGRP gene.
 A:Reference number: S07643; MUID:89386053
 A:Accession: S07644
 A:Molecule type: DNA
 A:Residues: 1-128 <BRO>
 A:Cross-references: EMBL:X15943; NID:929613; PIDN:CAA34070.1; PID:9296638
 A:Note: The authors translated the codon CAG for residue 19 as Glu
 R:Jonas, V.; Lin, C.R.; Kawashima, E.; Semon, D.; Swanson, L.W.; Mermod, J.J.; Evans, R.
 Proc. Natl. Acad. Sci. U.S.A. 82, 1998-2001, 1985
 A:Title: Alternative RNA processing events in human calcitonin/calcitonin gene-related
 A:Reference number: A94030; MUID:85166259
 A:Accession: A22949
 A:Molecule type: mRNA
 A:Residues: 1-128 <JON>
 A:Cross-references: GB:M12667; NID:9179825; PIDN:AAA51914.1; PID:9179828
 R:Edbrooke, M.R.; Parker, D.; McVey, J.H.; Riley, J.H.; Sorenson, G.D.; Pettengill, O.S.
 EMBO J. 4, 715-724, 1985
 A:Title: Expression of the human calcitonin/CGRP gene in lung and thyroid carcinoma.
 A:Reference number: A91034; MUID:85230541
 A:Accession: B22716
 A:Molecule type: mRNA
 A:Residues: 'V','50-75','S','76-128 <EDB>
 R:Steinberg, P.H.; Hoppener, J.W.; Zandberg, J.; Van de Ven, W.J.; Jansz, H.S.; Lips, C.
 J. Clin. Endocrinol. Metab. 59, 358-360, 1984
 A:Title: Calcitonin gene related peptide coding sequence is conserved in the human genom
 A:Reference number: I55336; MUID:84240176
 A:Accession: I55336
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 77-128 <RES>
 A:Cross-references: GB:M28637; NID:9180467; PIDN:AAA52012.1; PID:9457134
 R:Morris, H.R.; Panico, M.; Etienne, T.; Tipples, J.; Gargis, S.I.; MacIntyre, I.

Nature 308, 746-748, 1984
 A:Title: Isolation and characterization of human calcitonin gene-related peptide.
 A:Reference number: A93329; MUID:84191466
 A:Accession: J00005
 A:Molecule type: protein
 A:Residues: 83-119 <MOR>
 A:Note: this peptide was detected in medullary thyroid carcinoma tissue and in plasma
 R:Zaidi, M.; Brain, S.D.; Tipples, J.R.; di Marzo, V.; Moonagha, B.S.; Chambers, T.J.;
 Biochem. J. 269, 775-780, 1990
 A:Title: Structure-activity relationship of human calcitonin-gene-related peptide.
 A:Reference number: S10813; MUID:90358780
 A:Accession: S10813
 A:Molecule type: protein
 A:Residues: 83-99,'X','101-119 <ZAI>
 R:Pettermann, J.B.; Born, M.; Chang, J.Y.; Fischer, J.A.
 J. Biol. Chem. 262, 542-545, 1987
 A:Title: Identification in the human central nervous system, pituitary, and thyroid o
 A:Reference number: A92637; MUID:87109142
 A:Accession: A26142
 A:Molecule type: protein
 A:Residues: 83-88,'X','90-101','X','103-111','X','113-115','X','117 <P>
 R:Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
 Biochem. Biophys. Res. Commun. 185, 134-141, 1992
 A:Title: Isolation and characterization of peptides which act on rat platelets, from
 A:Reference number: JH0618; MUID:92287083
 A:Accession: JH0619
 A:Molecule type: protein
 A:Residues: 83,'X','85-88','X','90-108 <KIT>
 A:Experimental source: pheochromocytoma
 R:Nelkin, B.D.; Rosenfeld, K.I.; de Bustros, A.; Leong, S.S.; Roos, B.A.; Baylun, S.B
 Biochem. Biophys. Res. Commun. 123, 648-655, 1984
 A:Title: Structure and expression of a gene encoding human calcitonin and calcitonin
 A:Reference number: I52204; MUID:85022523
 A:Accession: I52204
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 48-119 <RE2>
 A:Cross-references: GB:K03512; NID:9180465; PIDN:AAA52011.1; PID:9180466
 R:Craig, R.K.; Riley, J.H.; Edbrooke, M.R.; Broad, P.M.; Foord, S.M.; Al-Kazwini, S.J
 Biochem. Soc. Symp. 52, 91-105, 1986
 A:Title: Expression and function of the human calcitonin/alpha-CGRP gene in health an
 A:Reference number: I39387; MUID:87213363
 A:Accession: I84508
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 77-128 <RE3>
 A:Cross-references: GB:M6094; NID:9179798; PIDN:AAA51912.1; PID:9179799
 C:Comment: This peptide is a potent vasorelaxant.
 C:Comment: This peptide increases the rate and force of contraction of rat auricles 1
 C:Genetics:
 A:Gene: GDB:CALCA; CALC1
 A:Cross-references: GDB:120571; OMIM:114130
 A:Map position: 11p15.2-11p15.1
 A:Introns: 29/2; 76/2
 C:Superfamily: calcitonin
 C:Keywords: alternative splicing; amidated carboxyl end; neuropeptide; vasodilator
 F:83-119/Product: calcitonin gene-related peptide alpha #status experimental <CTR>
 F:84-89/Disulfide bonds: #status experimental
 F:119/Modified site: amidated carboxyl end (Phe) (amide in mature form from following

Query Match 85.7%; Score 128.5; DB 1; Length 128;
 Best Local Similarity 90.0%; Pred. No. 1,3e-11;
 Matches 27; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRAGLLSRSGGWKSNFVPTNYSKAF 30
 |||||
 DB 91 THRAGLLSRSGGWKSNF-VPTNYSKAF 119

RESULT 4
 JH0709
 calcitonin gene-related peptide - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 08-Dec-1995
 C:Accession: JH0709
 R: Miyata, A.; Jiang, L.; Minamino, N.; Arimura, A.
 Biochem. Biophys. Res. Commun. 187, 1474-1479, 1992
 A:Title: Identification of calcitonin gene related peptide in ovine hypothalamic extract
 A:Reference number: JH0709; MUID:93038624
 A:Accession: JH0709
 A:Molecule type: protein
 A:Residues: 1-37 <MT>
 A:Experimental source: hypothalamus
 C:Comment: This protein has adenylate cyclase stimulating activity.
 C:Superfamily: calcitonin
 C:Keywords: amidated carboxyl end; neuropeptide
 F:37/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 85.0%; Score 127.5; DB 2; Length 37;
 Best Local Similarity 90.0%; Pred. No. 4,5e-12;
 Matches 27; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGMYKSNFVPTNGSKAF 30
 |||||
 Db 9 THRLAGLSRSGGVYKDNF-VPTNGSQAF 37

RESULT 5
 TCRTR
 calcitonin gene-related peptide precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 24-Sep-1999
 C:Accession: A01524; B22949
 R: Amara, S.G.; Jonas, V.; Rosenfeld, M.G.; Ong, E.S.; Evans, R.M.
 Nature 298 240-244, 1982
 A:Title: Alternative RNA processing in calcitonin gene expression generates mRNAs encoding
 A:Reference number: A01524; MUID:82220111
 A:Accession: A01524
 A:Molecule type: mRNA
 A:Residues: 1-128 <AMA>
 A:Cross-references: GB:I29188; GB:I00714; GB:N00016; NID:g457368; PIDN:AA59682.1; PID:g
 R:Jonas, V.; Lin, C.R.; Kawashima, E.; Samson, D.; Swanson, L.W.; Mermod, J.J.; Evans, R.
 Proc. Natl. Acad. Sci. U.S.A. 82, 1994-1998, 1985
 A:Title: Alternative RNA processing events in human calcitonin/calcitonin gene-related F
 A:Reference number: A94030; MUID:85166259
 A:Accession: B22949
 A:Molecule type: mRNA
 A:Residues: 1-39, 'A', 40-49, 'L', 50-67, 70-128 <JON>
 C:Superfamily: calcitonin
 C:Keywords: alternative splicing; amidated carboxyl end; neuropeptide
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:83-119/Product: calcitonin gene-related peptide #status predicted <MAT>
 F:84-89/Disulfide bonds: #status predicted
 F:119/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gl

Query Match 82.3%; Score 123.5; DB 1; Length 128;
 Best Local Similarity 86.7%; Pred. No. 6,9e-11;
 Matches 26; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGMYKSNFVPTNGSKAF 30
 |||||
 Db 91 THRLAGLSRSGGVYKDNF-VPTNGSEAF 119

RESULT 6
 A44173
 calcitonin gene-related peptide beta precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Jan-1993 #sequence_revision 12-Mar-1993 #text_change 16-Jul-1999
 C:Accession: A44173; S18300
 R:Amara, S.G.; Arriza, J.L.; Leff, S.E.; Swanson, L.W.; Evans, R.M.; Rosenfeld, M.G.
 Science 229, 1094-1097, 1985
 A:Title: Expression in brain of a messenger RNA encoding a novel neuropeptide homologous

A:Reference number: A44173; MUID:85300490
 A:Accession: A44173
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-134 <AMA>
 A:Cross-references: GB:M11596; NID:g203232; PIDN:AAA40850.1; PID:g203233
 A:Note: the authors translated the codon AAA for residue 47 as Phe, and CGC for resid
 R:Wang, M.W.; Young, A.A.; Rink, T.J.; Cooper, G.J.S.
 FEBS Lett. 291, 195-198, 1991
 A:Title: (8-37)-CCRP antagonizes actions of amylin on carbohydrate metabolism in vit
 A:Reference number: S18300; MUID:92038032
 A:Accession: S18300
 A:Molecule type: protein
 A:Residues: 96-104, 'S', 106-112, 'N', 114-125 <MAN>
 C:Superfamily: calcitonin
 C:Keywords: neuropeptide

Query Match 81.7%; Score 122.5; DB 2; Length 134;
 Best Local Similarity 86.7%; Pred. No. 1e-10;
 Matches 26; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGMYKSNFVPTNGSKAF 30
 |||||
 Db 97 THRLAGLSRSGGVYKDNF-VPTNGSKAF 125

RESULT 7
 B44173
 calcitonin gene-related peptide alpha precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Jan-1993 #sequence_revision 12-Mar-1993 #text_change 16-Jul-1999
 C:Accession: B44173
 R:Amara, S.G.; Arriza, J.L.; Leff, S.E.; Swanson, L.W.; Evans, R.M.; Rosenfeld, M.G.
 Science 229, 1094-1097, 1985
 A:Title: Expression in brain of a messenger RNA encoding a novel neuropeptide homolog
 A:Reference number: A44173; MUID:85300490
 A:Accession: B44173
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-128 <MAA>
 A:Cross-references: GB:M11597; NID:g203226; PIDN:AAA40847.1; PID:g203227
 A:Note: the authors translated the codon CGC for residue 99 as Ser
 C:Superfamily: calcitonin
 C:Keywords: neuropeptide

Query Match 79.0%; Score 118.5; DB 2; Length 128;
 Best Local Similarity 83.3%; Pred. No. 3,8e-10;
 Matches 25; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGMYKSNFVPTNGSKAF 30
 |||||
 Db 91 THRLAGLSRSGGVYKDNF-VPTNGSEAF 119

RESULT 8
 TCRRP
 calcitonin gene-related peptide precursor - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 18-Jun-1999
 C:Accession: S00154; I50183; A24855
 R:Minvielle, S.; Cressent, M.; Delehay, M.C.; Segond, N.; Milhaud, G.; Jullienne, A.
 FEBS Lett. 223, 63-68, 1987
 A:Title: Sequence and expression of the chicken calcitonin gene.
 A:Reference number: S00153; MUID:88030046
 A:Accession: S00154
 A:Molecule type: DNA
 A:Residues: 1-125 <MIN>
 A:Cross-references: EMBL:X06311
 A:Note: the sequences of codons 31-33 and 34-38 are interchanged in this reference; t
 R:Lasmoles, F.; Jullienne, A.; Day, F.; Minvielle, S.; Milhaud, G.; Moukhtar, M.S.

	Query Match	73.7%	Score 110.5	DB 1	Length 125
Best Local Similarity	80.0%	Pred. No. 5.6e-09			
Matches 24	Conservative	2	Mismatches 3	Indels 1	Gaps 1
OY	1	THRLAGLSRSGGVKSNFVPTNGSKAF	30		
db	88	THRLADFLSRSGGVKNNFVPTNGSKAF	116		

RESULT 9
A48939
cellobiohydrolase 1-1 - basidiomycete (Phanerochaete chrysosporium)
C:Species: Phanerochaete chrysosporium
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 22-Jun-1999
C:Accession: A48939
R:Coverit, S.F.; Vanden Wymelenberg, A.; Cullen, D.
Appl. Environ. Microbiol. 58, 2168-2175, 1992.
A:Title: Structure, organization, and transcription of a cellobiohydrolase gene cluster
A:Reference number: A48939; M01D:92344372
A:Accession: A48939
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-449 <COV>
A:Cross-references: GB:X54411; GB:S40817; NID:g3130; PIDD:CAA38274.1; PID:g3131.
A:Note: sequence extracted from NCBI backbone (NCIN:109508, NCBI:P109509)
C:Superfamily: cellulose 1,4-beta-cellulobiosidase I; fungal cellulose-binding domain homc

```

Query Match          34.7%; Score 52; DB 2; Length 449;
Best Local Similarity 39.1%; Pred. No. 9.7;
Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY      8  LSRSGGVKSKSNFVPTNVGSKAP 30
      :: || :: || || || ::
Db      103 ITTSGSALRLQFVGTNIGSRVF 125

RESULT  10

I40059
htraA-like protein - Brucella abortus
C/Species: Brucella abortus
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 21-Jul-2000
C/Accession: I40059
R:/atum, F.M.; Chevillat, N.F.; Morfillt, D.
Microb. Pathog. 17, 23-36, 1994
A:/file: Cloning, characterization and construction of htra and htraA-like mutants of Bru
A:/reference number: I40059; PMID:95165950
A:/status: preliminary; translated from GB/EMBL/DBJ

```

Query Match	34.08;	Score 51;	DB 1;	Length 474;
Best Local Similarly	44.48;	Pred. No. 14;		
Matches 12; Conservative	4;	Mismatches 7;	Indels 4;	Gaps 1;

```
QY      3  RLAG----LLSRSGGMVYKSNFVPTNV 25
          ||| : ||||| | : ||| :
Db      230 RLIGINTAIYSRSGGSVGIGFAIPSNM 256
```

A:Accession: A13349
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-474 <KUR>
A:Cross-references: GB:AE008917, PIDN:AAL51964.1, PID:g17982723; GSPDB:GN001900
A:Experimental source: strain 16M

A:Gene: BMEI0783
A:Map position: 1
C:Superfamily: Helicobacter serine proteinase
C:Keywords: hydrolase; serine proteinase

Query Match	34.0%;	Score 51;	DB 2;	Length 474;
Best Local Similarity	44.4%;	Pred. No. 14;		
Matches 12; Conservative	4;	Mismatches 7;	Indels 4;	Gaps 1;

```
QY      3  RLAG----LLSRSGMVKSNFVPTNV  25
          || : |||| | | : : || :
Db      230 RLGINTAIYSRSGSVGIGFAIPSNM  25
```

RESULT 12
A33542

C:Species: Felis silvestris catus (domestic cat)
C:Date: 21-Feb-1990 #sequence_revision 21-Feb-1990 #text_change 16-Jul-1999
C:Accession: A33542: A60499; B26619
R:Nish, M., Chan, S.-J., Negamatsu, S., Bell, G.I., Steiner, D.F.
Proc. Natl. Acad. Sci. U.S.A. 86, 5738-5742, 1989
A>Title: Conservation of the sequence of islet amyloid polypeptide in five mammals
X:Reference number: A33542; MIMD:89345542

A: Molecule type: mRNA
A: Residues: 189 <NTS>
A: Cross-references: GB:M25388; NID:g163861; PIDN:AAA30813.1; PID:g163862
R: Betsholtz, C.; Christmansson, L.; Engström, U.; Rotstein, F.; Jordan, K.; O'Brien, T.
Diabetes 39, 118-122, 1990
A: Title: Structure of cat islet amyloid polypeptide and identification of amino acid
A: Reference number: A60499; MUID:91006862
A: Accession: A60499
A: Status: not compared with conceptual translation
A: Molecule type: mRNA
A: Residues: 34-70 <BET>
R: Westermarck, P.; Wernstedt, C.; Wilander, E.; Hayden, D.W.; O'Brien, T.D.; Johnson,
Proc. Natl. Acad. Sci. U.S.A. 84, 3881-3885, 1987
A: Title: Amyloid fibrils in human insulinoma and islets of Langerhans of the diabetic

A:Reference number: A26619; MUID:87231921
A:Accession: B26619
A:Status: preliminary
A:Molecule type: protein
A:Residues: 34, 'X', 36-39, 'X', 41-60 <MES>
C:Superfamily: calcitonin
C:Keywords: amidated carboxyl end; amyloid; pancreas
F:70/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly

Query Match 33.7%; Score 50.5; DB 2; Length 89;
Best Local Similarity 43.3%; Pred. No. 2.7;
Matches 13; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGWVKSNEFVPTNVGSKAF 30
| | | | | : : : | | | | :
Db 42 TORLANFLIRSSNMLGA-ILSPTNVGSNTY 70

RESULT 13
A56855
Islet amyloid polypeptide precursor - chicken
N:Alternate names: INPP
C:Species: Gallus gallus (chicken)
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 16-Jul-1999
C:Accession: A56855
R:Fan, L.; Westermarck, G.; Chan, S.J.; Steiner, D.F.
Mol. Endocrinol. 8, 713-721, 1994
A:Title: Altered gene structure and tissue expression of islet amyloid polypeptide in th
A:Reference number: A56855; MUID:95021303
A:Accession: A56855
A:Status: preliminary
A:Molecule type: mRNA; DNA
A:Residues: 1-135 <FAN>
A:Cross-references: GB:JL6955; NID:g289789; PIDN:AAA67704.1; PID:g289790
C:Superfamily: calcitonin
C:Keywords: hormone

Query Match 33.7%; Score 50.5; DB 2; Length 135;
Best Local Similarity 43.3%; Pred. No. 4.3;
Matches 13; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGWVKSNEFVPTNVGSKAF 30
| | | | | : : : | | | | :
Db 88 TORLADFLVRSSNMGATY-SPTNVGSNTY 116

RESULT 14
T04301
beta-expansin - rice
C:Species: Oryza sativa (rice)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-May-2000
C:Accession: T04301
R:Cosgrove, D.J.; Bedinger, P.; Duracko, D.M.
Proc. Natl. Acad. Sci. U.S.A. 94, 6559-6564, 1997
A:Title: Group I allergens of grass pollen as cell wall-loosening agents.
A:Reference number: Z15266; MUID:97322412
A:Accession: T04301
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-261 <COS>
A:Cross-references: EMBL:U95968; NID:g2224914; PIDN:AAB61710.1; PID:g2224915
C:Superfamily: expansin

Query Match 33.0%; Score 49.5; DB 2; Length 261;
Best Local Similarity 39.5%; Pred. No. 12;
Matches 15; Conservative 5; Mismatches 7; Indels 11; Gaps 2;

OY 2 HRLAG-----LISRGWVKSNEFVPTNVGSK 28
| | | | | : | | | : | | | : | | | :
Db 220 HRLGPFSLRWVSESGQTVIAHOVIAPANWRANTVNGSK 257

RESULT 15
A24434
beta fimbrial protein precursor - Moraxella bovis
N:Alternate names: beta pillin
C:Species: Moraxella bovis
C:Date: 08-Aug-1987 #sequence_revision 08-Aug-1987 #text_change 26-Aug-1999
C:Accession: A24434; JI0072
R:Marrs, C.F.; Schoolnik, G.; Koomey, J.M.; Hardy, J.; Rothbard, J.; Falkow, S.
J. Bacteriol. 163, 132-139, 1985
A:Reference number: A24434; MUID:85234350
A:Accession: A24434
A:Molecule type: DNA
A:Residues: 1-157 <MAR>
A:Cross-references: GB:M11435; NID:g149760; PIDN:AAA25304.1; PID:g149761
A:Experimental source: strain EPP63
R:Ruethl, W.W.; Marrs, C.F.; Fernandez, R.; Falkow, S.; Schoolnik, G.K.
J. Exp. Med. 168, 983-1002, 1988
A:Title: Purification, characterization, and pathogenicity of Moraxella bovis pill.
A:Reference number: JI0071; MUID:89010522
A:Accession: JI0072
A:Molecule type: protein
A:Residues: 7-86, 93-122 <RUE>
A:Note: about 50% of the amino-terminus is N-methylated; the remaining 50% of the mol
C:Superfamily: gonococcal fimbrial protein
C:Keywords: methylated amino end; surface antigen
F:1-6/Domain: propenptide #status predicted <PRO>
F:1-157/Product: beta fimbrial protein 1 #status experimental <MAT>
F:8-157/Product: beta fimbrial protein 2 #status experimental <MA2>
F:7/Modified site: methylated amino end (Phe) (in mature form) #status experimental
F:136-155/Disulfide bonds: #status experimental

Query Match 32.7%; Score 49; DB 2; Length 157;
Best Local Similarity 39.1%; Pred. No. 8.4;
Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 8 LSRSGWVKSNEFVPTNVGSKAF 30
| : | | | : | | | : | | | :
Db 78 LTTTGTATSNLMSSVNTGGAF 100

Search completed: August 26, 2002, 15:52:37
Job time: 129 sec

1111

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 26, 2002, 15:50:48 ; Search time 25.2 Seconds
(without alignments)
205.946 Million cell updates/sec

Title: US-09-813-345-2

Perfect score: 150
Sequence: 1 THRLAGLSRSGWVKNFVPTNVGSKAF 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeop:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	124.5	83.0	128	6	Q9MYV1
2	123.5	82.3	128	11	Q99JAO
3	122.5	81.7	129	6	Q9NCT3
4	116.5	77.7	67	6	Q9GAK2
5	109.5	73.0	52	13	P79814
6	108.5	72.3	130	11	Q99MP3
7	106.5	71.0	56	13	Q92164
8	105.5	70.3	60	6	Q9GLK1
9	101.5	67.7	53	13	Q90YC3
10	78.5	52.3	127	6	Q9NOT2
11	36	37.3	223	5	Q9V9B4
12	52	34.7	144	11	Q9WVF6
13	52	34.7	407	2	Q9FC90
14	52	34.7	449	3	Q01762
15	52	34.7	605	5	Q9VM60
16	51	34.0	474	2	Q44596

17	50.5	33.7	135	13	Q90743	Q90743 gallus gall
18	50.5	33.7	4003	2	Q9RFLO	Q9RFLO stigmatella
19	49.5	33.0	261	10	Q9AV20	Q9AV20 oryza sativ
20	49.5	33.0	261	10	Q24230	Q24230 oryza sativ
21	49	32.7	190	5	Q25180	Q25180 heliopsis v
22	49	32.7	388	2	Q9E066	Q9E066 escherichia
23	49	32.7	388	2	Q9F6H3	Q9F6H3 escherichia
24	49	32.7	388	2	Q9F6H1	Q9F6H1 escherichia
25	49	32.7	1029	2	Q52708	Q52708 rickettsia
26	48.5	32.3	834	2	Q52647	Q52647 rickettsia
27	48	32.0	343	2	Q9F6H4	Q9F6H4 escherichia
28	48	32.0	388	2	Q9F6G8	Q9F6G8 escherichia
29	48	32.0	388	2	Q9F6G6	Q9F6G6 escherichia
30	48	32.0	388	2	Q9F6G4	Q9F6G4 escherichia
31	48	32.0	388	2	Q9F6G3	Q9F6G3 escherichia
32	48	32.0	388	2	Q9F6G2	Q9F6G2 escherichia
33	48	32.0	388	2	Q9F6G1	Q9F6G1 escherichia
34	48	32.0	388	2	Q9F6F9	Q9F6F9 escherichia
35	48	32.0	388	2	Q9F6F7	Q9F6F7 escherichia
36	48	32.0	388	2	Q9F6F5	Q9F6F5 escherichia
37	48	32.0	388	2	Q9F6F4	Q9F6F4 escherichia
38	48	32.0	388	2	Q9F6F3	Q9F6F3 escherichia
39	48	32.0	388	2	Q9F6F2	Q9F6F2 escherichia
40	48	32.0	875	2	Q86174	Q86174 bacteroides
41	47.5	31.7	336	10	Q944F5	Q944F5 oryza sativ
42	47.5	31.7	385	16	Q97EP2	Q97EP2 clostridium
43	47	31.3	428	16	Q98N31	Q98N31 rhizobium l
44	47	31.3	694	10	Q9LSC3	Q9LSC3 arabidopsis
45	47	31.3	995	16	Q9HY75	Q9HY75 pseudomonas

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	128 AA.
Q9MYV1	Q9MYV1	Q9MYV1		
AC	Q9MYV1	Q9MYV1		
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)			
DE	PREPRO-ALPHA-CALCITONIN GENE-RELATED PEPTIDE PRECURSOR.			
GN	CCALCT.			
OS	Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
OX	NCBI_TaxID=9615;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE-20353881; PubMed-10895326;			
RA	Wende S., Krempner A., Brenig B.;			
RT	"Detection of a polymorphic 27 bp insertion/deletion in exon 4 of the			
RL	canine calcitonin/calcitonin gene-related peptide gene 1.";			
RL	Anim. Genet. 31:238-239(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE-20424786; PubMed-10967131;			
RA	Wende S., Krempner A., Breen M., Brunberg L., Brenig B.;			
RT	"Molecular analysis and chromosomal assignment of the canine CALC-			
RT	I/alpha-CGRP gene.";			
RL	Mamm. Genome 11:736-740(2000).			
DR	EMBL; AJ271090; CAB97487.1; "			
DR	InterPro: IPR002163; Calcitonin beta.			
DR	InterPro: IPR001693; Calc CGRP IAPP.			
DR	InterPro: IPR000443; Islet amyloid.			
DR	Pfam; PF00214; Calc_CGRP_IAPP; 1.			
DR	PRINTS; PR00817; CALCITONINB.			
DR	PRINTS; PR00818; ISLETAMYLLOID.			
DR	SMART; SM00113; CALCITONIN; 1.			
KW	PROSITE; PS00258; CALCITONIN; 1.			
FT	SIGNAL.			
FT	SIGNAL	1	84	POTENTIAL.
FT	SIGNAL	1	82	POTENTIAL.

FT CHAIN 83 128 ALPHA-CALCITONIN GENE-RELATED PEPTIDE.
SQ SEQUENCE 128 AA; 13874 MW; 72331258DB8CB564 CRC64;

Query Match 83.0%; Score 124.5; DB 6; Length 128;
Best Local Similarity 86.7%; Pred. No. 2,8e-11;
Matches 26; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGVMKSNFVPTNVGSKAF 30
Db 91 THRLAGLSRSGVMKSNF-VPTNVGSEAF 119

RESULT 2

O99JAO PRELIMINARY; PRT; 128 AA.
AC O99JAO; 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DR 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE ALPHA-TYPE CALCITONIN GENE-RELATED PEPTIDE PRECURSOR.
CN CALCA OR CALC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Catalan J., Aramayo J., Sorribas V.;
RT "Mouse CGRP precursor is highly homologous to that of the rat.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVEV;
RA Thomas P.M., Nasonkin I., Zhang H., Gagel R.F., Cote G.J.;
RT "Structure of the Mouse Calcitonin/Calcitonin Gene-Related Peptide
RT Alpha and Beta Genes.";
RL DNA Seq. 0:0-0(2001).
DR EMBL; AF330212; AAK06841.1; -;
DR EMBL; AF335522; AAK18181.1; -;
DR EMBL; AF335521; AAK18181.1; JOINED.
MGI:2151253; Calca.
DR InterPro: IPR002163; Calcitonin_beta.
DR InterPro: IPR001693; Calc_CGRP_IAPP.
DR InterPro: IPR000443; Islet_amyloid.
DR Pfam: PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00817; CALCITONINB.
DR PRINTS; PR00818; ISLETAMYLTD.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
FT CHAIN 83 119 ALPHA-TYPE CALCITONIN GENE-RELATED
FT PEPTIDE PRECURSOR.
SQ SEQUENCE 128 AA; 14065 MW; 83BB0E36C8B4239E CRC64;

Query Match 82.3%; Score 123.5; DB 11; Length 128;
Best Local Similarity 86.7%; Pred. No. 4e-11;
Matches 26; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGVMKSNFVPTNVGSKAF 30
Db 91 THRLAGLSRSGVMKSNF-VPTNVGSEAF 119

RESULT 3

O9N0T3 PRELIMINARY; PRT; 129 AA.
AC O9N0T3; 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DR 01-OCT-2000 (TREMblrel. 17, Last annotation update)
DE CALCITONIN GENE RELATED PEPTIDE II PRECURSOR.
CN Equus caballus (Horse).
OS Equus caballus (Horse).
FT CHAIN 83 129
FT PEPTIDE PRECURSOR.
SQ SEQUENCE 129 AA; 13925 MW; 97C2C7AC713ABD9B CRC64;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Toribio R.E., Kohn C.W., Chew D.J., Rosol T.J.;
RT "Molecular Cloning of Equine Calcitonin and Calcitonin Gene Related
RT Peptide.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF257470; AAF70199.1; -;
DR InterPro: IPR002163; Calcitonin_beta.
DR InterPro: IPR001693; Calc_CGRP_IAPP.
DR InterPro: IPR000443; Islet_amyloid.
DR Pfam: PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00817; CALCITONINB.
DR PRINTS; PR00818; ISLETAMYLTD.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
KW Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 84 120 CALCITONIN GENE RELATED PEPTIDE II.
FT SEQUENCE 129 AA; 13925 MW; 97C2C7AC713ABD9B CRC64;

Query Match 81.7%; Score 122.5; DB 6; Length 129;
Best Local Similarity 86.7%; Pred. No. 5,8e-11;
Matches 26; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGVMKSNFVPTNVGSKAF 30
Db 92 THRLAGLSRSGVMKSNF-VPTNVGSEAF 120

RESULT 4

O9GLK2 PRELIMINARY; PRT; 67 AA.
AC O9GLK2; 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DR 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE CALCITONIN GENE-RELATED PEPTIDE VARIANT 1 (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Davis M.C., Gierasch W.W., Russo A.F.;
RT "Rabbit calcitonin gene-related peptide partial cDNA for exons 3 and
RT 5, variant allele 1.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF260272; AAG15535.1; -;
DR InterPro: IPR002163; Calcitonin_beta.
DR InterPro: IPR001693; Calc_CGRP_IAPP.
DR InterPro: IPR000443; Islet_amyloid.
DR Pfam: PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00817; CALCITONINB.
DR PRINTS; PR00818; ISLETAMYLTD.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
FT NON_TER 1 67
FT NON_TER 1 67
SQ SEQUENCE 67 AA; 7286 MW; 99CG326C159BC501 CRC64;

Query Match 77.7%; Score 116.5; DB 6; Length 67;
Best Local Similarity 96.2%; Pred. No. 2,3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGVMKSNFVPTNVG 26
Db 42 THRLAGLSRSGVMKSNF-VPTNVG 66


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RESULT 5
P79814 PRELIMINARY; PRT; 52 AA.
ID P79814
AC P79814
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CALCITONIN GENE-RELATED PEPTIDE 4 (FRAGMENT).
OS Oncorhynchus gorbuscha (Pink salmon) (Humpback salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OK NCBI_TaxID=8017;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97057244; PubMed=8901583;
RA Jansz H., Martial K., Zandberg J., Milnaud G., Benson A.A.,
RA Juliette A., Moukhtar M.S., Cressent M.;
RT "Identification of a new calcitonin gene in the salmon Oncorhynchus
RT gorbuscha.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:12344-12348(1996).
DR EMBL: U71287; AAB38533.1; -.
DR InterPro: IPR002163; Calcitonin_beta.
DR InterPro: IPR001693; Calc_CGRP_IAPP.
DR Pfam: PF00214; Calc_CGRP_IAPP.
DR PRINTS: PR00817; CALCITONINB.
DR SMART: SM00113; CALCITONIN.
DR PROSITE: PS00258; CALCITONIN.
FT NON_TER 1 1
FT CHAIN 1 4 N-TERMINAL PEPTIDE.
FT CHAIN 7 43 CALCITONIN GENE-RELATED PEPTIDE 4.
FT CHAIN 52 CARBOXY TERMINAL PEPTIDE.
SQ SEQUENCE 52 AA; 5700 MW; 3F4C471D2A682321 CRC64;

Query Match 73.0%; Score 109.5; DB 13; Length 52;
Best Local Similarity 80.0%; Pred. No. 2e-09;
Matches 24; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 THRAGLLSRSGGMVKSNEVPTNGSKAF 30
Db 15 THRAGLLSRSGGMVKSNEVPTNGSKAF 43

RESULT 6
Q99MP3 PRELIMINARY; PRT; 130 AA.
ID Q99MP3
AC Q99MP3
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CALCITONIN/CALCITONIN-RELATED PEPTIDE BETA.
GN CALCB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVEV;
RA Thomas P.W., Nasonkin I., Zhang H., Gagel R.F., Cote G.J.;
RT "Structure of the Mouse Calcitonin/Calcitonin Gene-Related Peptide
RT Alpha and Beta Genes.";
RL DNA Seq. 0:0-0(2001).
DR EMBL: AF325526; AAK16431.1; -.
DR EMBL: AF325524; AAK16431.1; JOINED.
DR MGD; MGI:2151254; Calcd.
DR InterPro: IPR002163; Calcitonin_beta.
DR InterPro: IPR001693; Calc_CGRP_IAPP.
DR InterPro: IPR000443; Islet amyloid.
DR Pfam: PF00214; Calc_CGRP_IAPP.
DR PRINTS: PR00817; CALCITONINB.

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DR PRINTS: PR00818; ISLETAMYLOID.
DR SMART: SM00113; CALCITONIN.
DR PROSITE: PS00258; CALCITONIN.
SQ SEQUENCE 130 AA; 14623 MW; 97299244EBF6C536 CRC64;

Query Match 72.3%; Score 108.5; DB 11; Length 130;
Best Local Similarity 76.7%; Pred. No. 8e-09;
Matches 23; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 THRAGLLSRSGGMVKSNEVPTNGSKAF 30
Db 92 THRAGLLSRSGGMVKSNEVPTNGSKAF 120

RESULT 7
Q92164 PRELIMINARY; PRT; 56 AA.
ID Q92164
AC Q92164
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CALCITONIN GENE-RELATED PEPTIDE (FRAGMENT).
GN CGRP.
OS Oncorhynchus sp. (Salmon).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OK NCBI_TaxID=8025;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92344325; PubMed=1637123;
RA Jansz H.S., Zandberg J.;
RT "Identification and partial characterization of the salmon
RT calcitonin/CGRP gene by polymerase chain reaction.";
RL Ann. N.Y. Acad. Sci. 657:63-69(1992).
DR EMBL: S40497; AAB22593.1; -.
DR InterPro: IPR002163; Calcitonin_beta.
DR InterPro: IPR001693; Calc_CGRP_IAPP.
DR Pfam: PF00214; Calc_CGRP_IAPP.
DR PRINTS: PR00817; CALCITONINB.
DR SMART: SM00113; CALCITONIN.
DR PROSITE: PS00258; CALCITONIN.
FT NON_TER 1 1
SQ SEQUENCE 56 AA; 6019 MW; C7852837BAF74314 CRC64;

Query Match 71.0%; Score 106.5; DB 13; Length 56;
Best Local Similarity 76.7%; Pred. No. 6.4e-09;
Matches 23; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 THRAGLLSRSGGMVKSNEVPTNGSKAF 30
Db 15 THRAGLLSRSGGMVKSNEVPTNGSKAF 43

RESULT 8
Q9GLK1 PRELIMINARY; PRT; 60 AA.
ID Q9GLK1
AC Q9GLK1
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CALCITONIN GENE-RELATED PEPTIDE (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Davis M.C., Giersch W.W., Russo A.F.;
RT "Rabbit calcitonin gene-related peptide partial cDNA for exons 3 and
RT 5.";

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RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF260273; AAC15536.1;
DR InterPro: IPR002163; Calcitonin_beta.
DR InterPro: IPR001693; Calc_CGRP_IAPP.
DR InterPro: IPR000443; Islet_Amyloid.
DR Pfam: PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS: PR00817; CALCITONINB.
DR SMART: SM00113; CALCITONIN; 1.
DR PROSITE: PS00258; CALCITONIN; 1.
FT NON_TER 1
FT CHAIN 60
FT SEQUENCE 60 AA: 6485 MW: 5D8A512A4E8994AE CRC64;

Query Match
Best Local Similarity 70.3%; Score 105.5; DB 6; Length 60;
Matches 23; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 THRLAGLSRSGMKVSNFVPTNVG 26
DB 35 THRLADLLSRSGVYKSNF-VPTNVG 59

RESULT 9
QY0YC3 PRELIMINARY; PRT; 53 AA.
AC QY0YC3:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CALCITONIN GENE-RELATED PEPTIDE (FRAGMENT).
OS Paratichthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neuteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paratichthyidae; Paratichthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21406117; PubMed=11514025;
RA Suzuki N., Suzuki T., Kurokawa T.;
RT "Cloning of a calcitonin gene-related peptide from genomic DNA and its
RT mRNA expression in flounder, Paratichthys olivaceus.";
RL Peptides 22:1435-1438(2001).
DR EMBL: AB052782; BAB64411.1;
FT NON_TER 1
FT CHAIN 60
FT SEQUENCE 53 AA: 5684 MW: 14C0191868A64CF4 CRC64;

Query Match
Best Local Similarity 67.7%; Score 101.5; DB 13; Length 53;
Matches 22; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 1 THRLAGLSRSGMKVSNFVPTNVGSKAF 30
DB 16 THRLADLLSRSGLGYNMF-VPTNVGAQAF 44

RESULT 10
QY0NT2 PRELIMINARY; PRT; 127 AA.
AC QY0NT2:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CALCITONIN GENE RELATED PEPTIDE I PRECURSOR.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;

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RN [1]
RP SEQUENCE FROM N.A.
RA Toribio R.E., Kohn C.W., Chew D.J., Rosol T.J.;
RT "Molecular Cloning of Equine Calcitonin and Calcitonin-Gene Related
RT Peptides.";
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF251471; AAF70200.1;
DR InterPro: IPR002163; Calcitonin_beta.
DR InterPro: IPR001693; Calc_CGRP_IAPP.
DR InterPro: IPR000443; Islet_Amyloid.
DR Pfam: PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS: PR00817; CALCITONINB.
DR PRINTS: PR00818; ISLETAMYL0ID.
DR SMART: SM00113; CALCITONIN; 1.
FT SIGNAL 1
FT CHAIN 82
FT SEQUENCE 127 AA: 13864 MW: BA570B2AB49A6730 CRC64;

Query Match
Best Local Similarity 52.3%; Score 78.5; DB 6; Length 127;
Matches 17; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 THRLAGLSRSGMKVSNFVPTNVGSK 28
DB 90 THRLAGLSRSGMANSN-LTPTEMGFK 116

RESULT 11
QY9B4 PRELIMINARY; PRT; 223 AA.
AC QY9B4:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CG3403 PROTEIN.
GN CG3403.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burlis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Modyanov C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleib J.M.,

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Search completed: August 26, 2002, 15:53:09
Job time: 141 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 26, 2002, 15:51:24 ; Search time 10.42 Seconds
(without alignments)
111.477 Million cell updates/sec

Title: US-09-813-345-2

Perfect score: 150
Sequence: 1 THRAGLSRSGMKSNFYVPTNYGSKAF 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	135.5	90.3	127	1 CAL2_HUMAN	P10092 homo sapien
2	128.5	85.7	128	1 CAL1_HUMAN	P06881 homo sapien
3	127.5	85.0	37	1 CGRP_SHEEP	P30881 ovis aries
4	126.5	84.3	37	1 CGRP_PIG	P03880 sus scrofa
5	123.5	82.3	128	1 CAL1_RAT	P01256 rattus norv
6	122.5	81.7	134	1 CAL2_RAT	P10093 rattus norv
7	117.5	78.3	37	1 CGRP_RANRI	P31888 rana ridibn
8	110.5	73.7	125	1 CALR_CHICK	P10286 gallus gall
9	68.5	45.7	115	1 CGRP_PHYBI	P11564 phyllomedus
10	53.5	35.7	32	1 IAPP_SAGOE	Q28934 saguinus,oe
11	52	34.7	144	1 IAPP_MOUSE	Q28934 mus musculu
12	50.5	33.7	89	1 IAPP_FELCA	P12967 felis silve
13	49	32.7	157	1 FMO_MORBO	P07640 moraxella b
14	49	32.7	516	1 GUX1_PNACH	P13860 phanerocha
15	48.5	32.3	93	1 IAPP_MOUSE	P12968 mus musculu
16	48.5	32.3	93	1 IAPP_RAT	P12969 rattus norv
17	48	32.0	428	1 THRC_ECOLI	P00934 escherichia
18	48	32.0	429	1 OGRA_MYCU	O10387 mycobacteri
19	48	32.0	533	1 PRG_BORBU	O51522 borrelia bu
20	48	32.0	1609	1 RRPQ_TMGNV	P18339 tobacco mil
21	48	32.0	2021	1 OMPA_RICCN	Q22657 ticketstia
22	47.5	31.7	89	1 IAPP_CANFA	P17716 canis famli
23	47	31.3	833	1 PTIA_ECOLI	P32670 escherichia
24	46.5	31.0	230	1 EBP_MOUSE	P70245 mus musculu
25	46	30.7	258	1 ARGH_BACSU	P36840 bacillus su
26	46	30.7	434	1 Y181_MYCN	O50292 mycoplasma
27	46	30.7	2249	1 OMPA_RICCN	P18921 ticketstia
28	45.5	30.3	37	1 IAPP_CRIGR	P19890 cricetus
29	45.5	30.3	92	1 IAPP_MESAU	P23442 mesocricetu
30	45	30.0	159	1 MYFA_YEREN	P33406 yersinia en
31	45	30.0	242	1 HYPB_HELPJ	O92560 helicobacte
32	45	30.0	242	1 HYPB_HELPJ	O92560 helicobacte
33	45	30.0	429	1 THRC_BUCAL	P57289 buchnera ap

34	45	30.0	489	1 CPCU_RABIT	Q29510 oryctolagus
35	45	29.7	748	1 JSB1_TRINI	Q06342 trichoplusi
36	44.5	29.7	522	1 GSHL_ARATH	P46309 arabidopsis
37	44.5	29.7	3023	1 POLG_TYMU	P09814 t genome po
38	44	29.3	429	1 THRC_SERMA	P27735 serratia ma
39	44	29.3	439	1 RCA2_TOBAC	Q40565 nicotiana t
40	44	29.3	442	1 RCA1_TOBAC	Q40460 nicotiana t
41	44	29.3	575	1 IIVB_IACLA	Q02137 lactococcus
42	44	29.3	1116	1 VP2_RDVF	Q98632 rice dwarf
43	44	29.3	1222	1 PM5P_HUMAN	Q15155 homo sapien
44	44	29.3	1612	1 RRPQ_ORSVS	Q64133 odontogloss
45	44	29.3	2491	1 MPRL_HUMAN	P11717 homo sapien

ALIGNMENTS

RESULT	1	STANDARD	PRT	127 AA
ID	CAL2_HUMAN			
AC	P10092; O9GCM9;			
DT	01-MAR-1989 (rel. 10, Created)			
DT	01-MAR-1989 (rel. 10, Last sequence update)			
DT	16-OCT-2001 (rel. 40, Last annotation update)			
DE	Calcitonin gene-related peptide II precursor (CGRP-II) (Beta-type CGRP).			
DE	CALCB OR CALC2.			
GN	Calcitonin (Human).			
OS	Human sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87105923; PubMed=3492393;			
RA	Steenbergh P.H., Hoepfner J.W.M., Zandberg J., Vlasser A.,			
RA	Lips C.J.M., Jansz H.S.;			
RT	"Structure and expression of the human calcitonin/CGRP genes.";			
RL	FEBS Lett. 209:97-103(1986).			
RN	[2]			
RP	SEQUENCE OF 56-127 FROM N.A.			
RX	MEDLINE=85180007; PubMed=2985435;			
RA	Steenbergh P.H., Hoepfner J.W.M., Zandberg J., Lips C.J.M.,			
RA	Jansz H.S.;			
RT	"A second human calcitonin/CGRP gene.";			
RL	FEBS Lett. 183:403-407(1985).			
RN	[3]			
RP	PARTIAL SEQUENCE OF 82-108.			
RX	MEDLINE=87109142; PubMed=3492492;			
RA	Petermann J.B., Born W., Chang J.Y., Fischer J.A.;			
RT	"Identification in the human central nervous system, pituitary, and			
RT	thyroid of a novel calcitonin gene-related peptide, and partial amino			
RT	acid sequence in the spinal cord.";			
RL	J. Biol. Chem. 262:542-545(1987).			
RN	[4]			
RP	SEQUENCE OF 82-86 AND 104-117.			
RX	TISSUE=Spinal cord;			
RC	TISSUE=Spinal cord;			
RA	MEDLINE=90211348; PubMed=2322288;			
RA	Wimalawansa S.J., Morris H.R., Etienne A., Blench I., Panico M.,			
RA	McIntyre I.;			
RT	"Isolation, purification and characterization of beta-hCGRP from			
RT	human spinal cord.";			
RL	Biochem. Biophys. Res. Commun. 167:993-1000(1990).			
RN	[5]			
RP	SEQUENCE OF 82-104.			
RX	TISSUE=Phenochromocytoma;			
RC	TISSUE=Phenochromocytoma;			
RA	MEDLINE=92287083; PubMed=1318039;			
RX	Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Matsuo H., Eto T.;			
RT	"Isolation and characterization of peptides which act on rat			
RT	platelets, from a pheochromocytoma.";			
RL	Biochem. Biophys. Res. Commun. 185:134-141(1992).			
CC	"-1- FUNCTION: CGRP INDUCES VASODILATION. IT DILATES A VARIETY OF			
CC	VESSELS INCLUDING THE CORONARY, CEREBRAL AND SYSTEMIC VASCULATURE.			
CC	ITS ABUNDANCE IN THE CNS ALSO POINTS TOWARD A NEUROTRANSMITTER OR			

CC NEURONMODULATOR ROLE.
 CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: X04855; CAC05295.1; -
 DR EMBL: X04857; CAC05295.1; JOINED.
 DR EMBL: X04861; CAC05295.1; JOINED.
 DR EMBL: X02404; CAC26249.1; -
 DR PIR: A25864; A25864.
 DR PIR: A34565; A34565.
 DR PIR: B26142; B26142.
 DR MIM: 114160; -
 DR InterPro: IPR001693; Calc-CGRP_IAPP.
 DR InterPro: IPR002163; Calcitonin_beta.
 DR Pfam: PF00214; Calc-CGRP_IAPP; 1.
 DR PRINTS: PR00817; CALCITONINB.
 DR SMART: SM00113; CALCITONINB.
 DR PROSITE: PS00256; CALCITONIN; 1.
 KW Cleavage on pair of basic residues; Amidation; Hormone; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT PROPEP 26 79
 FT PROPEP 82 118 CALCITONIN GENE-RELATED PEPTIDE II.
 FT PROPEP 124 127
 FT DISULFID 83 88
 FT MOD_RES 118 118 AMIDATION (G-119 PROVIDE AMIDE GROUP).
 FT CONFLICT 73 73 G -> S (IN REF. 2).
 SQ SEQUENCE 127 AA; 13706 MW; B0A71A063CD5ACE7 CRC64;
 QY 1 THRLLGLLSRSGWVKSNFVPTNVGSKAF 30
 DB 90 THRLLGLLSRSGWVKSNF-VPTNVGSKAF 118
 RESULT 2
 ID CALI_HUMAN STANDARD; PRT; 128 AA.
 AC P06881; Q93048; Q9UCP0;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calcitonin gene-related peptide I precursor (CGRP-I) (Alpha-type
 DE CGRP).
 GN CALCA OR CALCI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89386053; PubMed=2571128;
 RA Broad P.M., Symes A.J., Thakker R.V., Craig R.K.;
 RT "Structure and methylation of the human calcitonin/alpha-CGRP gene.";
 RL Nucleic Acids Res. 17:6599-7011(1989).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85166259; PubMed=3872459;
 RA Jones V., Lin C.R., Kawashima E., Semon D., Swanson L.W.,
 RA Mermod J.-J., Evans R.M., Rosenfeld M.G.;
 RT "Alternative RNA processing events in human calcitonin/calcitonin
 RT gene-related peptide gene expression.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:1994-1998(1985).

RN (3)
 RP SEQUENCE OF 48-119 FROM N.A.
 RX MEDLINE=85022523; PubMed=6148938;
 RA Nelkin B.D., Rosenfeld K.I., de Bustros A., Leong S.S., Roos B.A.,
 RA Baylin S.B.;
 RT "Structure and expression of a gene encoding human calcitonin and
 RT calcitonin gene related peptide.";
 RL Biochem. Biophys. Res. Commun. 123:648-655(1984).
 RN (4)
 RP SEQUENCE OF 49-128 FROM N.A.
 RX MEDLINE=85230541; PubMed=2408883;
 RA Edbrooke M.R., Parker D., McVey J.H., Riley J.H., Sorenson G.D.,
 RA Pettengill O.S., Craig R.K.;
 RT "Expression of the human calcitonin/CGRP gene in lung and thyroid
 RT carcinoma.";
 RL EMBO J. 4:715-724(1985).
 RN (5)
 RP SEQUENCE OF 77-128 FROM N.A.
 RC TISSUE=Thyroid carcinoma;
 RX MEDLINE=84240176; PubMed=6610687;
 RA Steenberg P.H., Hoppe J.W., Zandberg J., de Ven W.J., Jansz H.S.,
 RA Lips C.J.;
 RT "Calcitonin gene related peptide coding sequence is conserved in the
 RT human genome and is expressed in medullary thyroid carcinoma.";
 RL J. Clin. Endocrinol. Metab. 59:358-360(1984).
 RN (6)
 RP SEQUENCE OF 77-128 FROM N.A.
 RX MEDLINE=87213363; PubMed=3034287;
 RA Craig R.K., Riley J.H., Edbrooke M.R., Broad P.M., Foord S.M.,
 RA Al-Kazwini S.J., Holman J.J., Marshall I.;
 RT "Expression and function of the human calcitonin/alpha-CGRP gene in
 RT health and disease";
 RL Biochem. Soc. Symp. 52:91-105(1986).
 RN (7)
 RP SEQUENCE OF 83-119.
 RX MEDLINE=84191466; PubMed=6609312;
 RA Morris H.R., Panico M., Etienne T., Tiplins J., Garg S.I.,
 RA McIntyre I.;
 RT "Isolation and characterization of human calcitonin gene-related
 RT peptide.";
 RL Nature 308:746-748(1984).
 RN (8)
 RP PARTIAL SEQUENCE OF 83-117.
 RX MEDLINE=87109142; PubMed=3492492;
 RA Petermann J.B., Born W., Chang J.Y., Fischer J.A.;
 RT "Identification in the human central nervous system, pituitary, and
 RT thyroid of a novel calcitonin gene-related peptide, and partial amino
 RT acid sequence in the spinal cord.";
 RL J. Biol. Chem. 262:542-545(1987).
 RN (9)
 RP SEQUENCE OF 83-108, AND FUNCTION.
 RC TISSUE=Phaeochromocytoma;
 RX MEDLINE=92287083; PubMed=1318039;
 RA Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Matsuo H., Eto T.;
 RT "Isolation and characterization of peptides which act on rat
 RT platelets, from a phaeochromocytoma.";
 RL Biochem. Biophys. Res. Commun. 185:134-141(1992).
 RN (10)
 RP STRUCTURE BY NMR OF CGRP.
 RX MEDLINE=91105142; PubMed=1988044;
 RA Breeze A.L., Harvey T.S., Bazzo R., Campbell I.D.;
 RT "Solution structure of human calcitonin gene-related peptide by 1H
 RT NMR and distance geometry with restrained molecular dynamics.";
 RL Biochemistry 30:575-582(1991).
 RN (11)
 RP STRUCTURE BY NMR OF CGRP.
 RX MEDLINE=91248117; PubMed=2039456;
 RA Hubbard J.A.M., Martin S.R., Chaplin L.C., Bose C., Kelly S.M.,
 RA Price N.C.;
 RT "Solution structures of calcitonin-gene-related-peptide analogues of
 RT calcitonin-gene-related peptide and amylin.";
 RL Biochem. J. 275:785-788(1991).
 CC -1- FUNCTION: CGRP induces vasodilatation. It dilates a variety of

vessels including the coronary, cerebral and systemic vasculature. Its abundance in the CNS also points toward a neurotransmitter or neuromodulator role. It also elevates platelet CAMP.

-1- ALTERNATIVE PRODUCTS: 3 ISOBFORMS: 1 (AC P01258), 2 (AC P01259) AND 3 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

-1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.

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DR EMBL; X15943; CA34070.1; -
DR EMBL; X02330; CA26190.1; -
DR EMBL; M12667; AA51914.1; -
DR EMBL; M12664; AA51914.1; JOINED.
DR EMBL; M12665; AA51914.1; JOINED.
DR EMBL; K03512; AA52011.1; -
DR EMBL; M28637; AA52012.1; -
DR EMBL; M26094; AA51912.1; -
DR PIR; B22716; TCHUR.
DR PIR; A22949; A22949.
DR PIR; A26142; A26142.
DR PIR; S07644; S07644.
DR MIM; I14130; -
DR InterPro; IPR001693; Calc_CGRP_IAPP.
DR InterPro; IPR002163; Calcitonin_beta.
DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00817; CALCITONINB.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
DR Cleavage on pair of basic residues; Amidation; Alternative splicing;
KM Hormone: Signal.
FT SIGNAL 1 25 POTENTIAL.
FT PROPEP 26 80
FT PEPTIDE 83 119 CALCITONIN GENE-RELATED PEPTIDE I.
FT PROPEP 125 128
FT DISULFID 84 89
FT MOD_RES 119 119 AMIDATION (G-120 PROVIDE AMIDE GROUP).
FT CONFLICT 48 48 R -> V (IN REF. 4).
FT CONFLICT 76 76 R -> V (IN REF. 3).
SQ SEQUENCE 128 AA; 13899 MW; A003A1069260D9B8 CRC64;

Query Match 85.7%; Score 128.5; DB 1; Length 128;
Best Local Similarity 90.0%; Pred. No. 1.9e-12;
Matches 27; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGVWKSNFVPTVNGSKAF 30
DB 91 THRLAGLSRSGVWKNF-VPTVNGSKAF 119

RESULT 3
CGRP_SHEEP STANDARD; PRT; 37 AA.
AC P30881;
DT 01-JUL-1993 (Rel. 26, Created)
DT 15-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Calcitonin gene-related peptide (CGRP).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_Taxid=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Hypothalamus;
RX MEDLINE=93038624; PubMed=1417824;

RA Miyata A., Jiang L., Minamino N., Arimura A.;
RT "Identification of calcitonin gene related peptide in ovine
RT hypothalamic extract."
RL Biochem. Biophys. Res. Commun. 187:1474-1479(1992).
CC -1- FUNCTION: CGRP INDUCES VASODILATION. IT DILATES A VARIETY OF
CC VESSELS INCLUDING THE CORONARY, CEREAL AND SYSTEMIC VASCULATURE.
CC ITS ABUNDANCE IN THE CNS ALSO POINTS TOWARD A NEUROTRANSMITTER OR
CC NEUROMODULATOR ROLE.
CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
CC PIR; JH0709; JH0709.
DR InterPro; IPR001693; Calc_CGRP_IAPP.
DR InterPro; IPR002163; Calcitonin_beta.
DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00817; CALCITONINB.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
DR Amidation; Hormone.
KW DISULFID 2
FT MOD_RES 37 37 BY SIMILARITY.
SQ SEQUENCE 37 AA; 3780 MW; F5DDE64D248B6A47 CRC64;

Query Match 85.0%; Score 127.5; DB 1; Length 37;
Best Local Similarity 90.0%; Pred. No. 7.4e-13;
Matches 27; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGVWKSNFVPTVNGSKAF 30
DB 9 THRLAGLSRSGVWKNF-VPTVNGSKAF 37

RESULT 4
CGRP_PIG STANDARD; PRT; 37 AA.
AC P30880;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Calcitonin gene-related peptide (CGRP).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=87173481; PubMed=3494209;
RA Kimura S., Sugita Y., Kanazawa I., Saito A., Goto K.;
RT "Isolation and amino acid sequence of calcitonin gene related peptide
RT from porcine spinal cord."
RL Neuropeptides 9:75-82(1987).
CC -1- FUNCTION: CGRP INDUCES VASODILATION. IT DILATES A VARIETY OF
CC VESSELS INCLUDING THE CORONARY, CEREAL AND SYSTEMIC VASCULATURE.
CC ITS ABUNDANCE IN THE CNS ALSO POINTS TOWARD A NEUROTRANSMITTER OR
CC NEUROMODULATOR ROLE.
CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
CC InterPro; IPR001693; Calc_CGRP_IAPP.
DR InterPro; IPR002163; Calcitonin_beta.
DR Pfam; PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS; PR00817; CALCITONINB.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
DR Amidation; Hormone.
KW DISULFID 2
FT MOD_RES 37 37 BY SIMILARITY.
SQ SEQUENCE 37 AA; 3814 MW; 04CDEB8D248B64BA CRC64;

Query Match 84.3%; Score 126.5; DB 1; Length 37;
Best Local Similarity 90.0%; Pred. No. 1.1e-12;
Matches 27; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGVWKSNFVPTVNGSKAF 30
DB 9 THRLAGLSRSGVWKNF-VPTVNGSKAF 37

QY	Db	1	THRLAGLLSRSGAMVSNFVPTNGSKAF	30
			:	116
		88	THRLADFLSRSGVGKNNP-VPTNGSKAF	116
RESULT	9			
CGRP_PHYBI				
CGRP_PHYBI				
STANDARD:				
PRT:	115	AA.		
Query Match	73.7%	Score	110.5;	DB 1;
Best Local Similarity	80.0%;	Pred. No.	9.9e-10;	Length 125;
Matches	24;	Conservative	2;	Mismatches 3;
				Indels 1;
				Gaps 1;

AC P81564;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Skin calcitonin gene-related peptide precursor (S-CGRP).
 OS Phylomedusa bicolor (Two-colored leaf frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Phylomedusa.
 NCBI_TaxID=8393;
 RN [1]
 RP SEQUENCE FROM N.A., SEQUENCE OF 70-106, AND CHARACTERIZATION.
 RC TISSUE-SKIN;
 RX MEDLINE=20148807; PubMed=10681586;
 RA Seon A.A., Pierre T.N., Redeker V., Lacombe C., Delfour A.,
 RA Nicolas P., Amiche M.;
 RT "Isolation, structure, synthesis, and activity of a new member of the
 RT calcitonin gene-related peptide family from frog skin and molecular
 RT cloning of its precursor".
 RL J. Biol. Chem. 275:5934-5940(2000).
 CC -1- FUNCTION: CGRP INDUCES VASODILATION. IT DILATES A VARIETY OF
 CC VESSELS INCLUDING THE CORONARY, CEREBRAL AND SYSTEMIC VASCULATURE.
 CC ITS ABUNDANCE IN THE CNS ALSO POINTS TOWARD A NEUROTRANSMITTER OR
 CC NEUROMODULATOR ROLE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: SKIN, INTERSTINE AND BRAIN.
 CC -1- MASS SPECTROMETRY: MW=3,806.77; METHOD=MALDI; RANGE=70-106.
 CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
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 CC -----
 DR EMBL: Y18495; CAB76385.1; -
 DR InterPro: IPR001693; Calc_CGRP_IAPP.
 DR InterPro: IPR002163; Calcitonin_beta.
 DR Pfam: PF00214; Calc_CGRP_IAPP; 1.
 DR PRINTS: PR00817; CALCITONINB.
 DR SMART: SM00113; CALCITONIN; 1.
 DR PROSITE: PS00258; CALCITONIN; 1.
 KW Signal; Cleavage on pair of basic residues; Amidation; Hormone;
 KW Amphibian skin.
 FT SIGNAL 1 25 POTENTIAL.
 FT PROPEP 26 69 REMOVED IN MATURE FORM BY
 FT CHAIN 70 106 CARBOXYPEPTIDASE.
 FT PROPEP 107 115 SKIN CALCITONIN GENE-RELATED PEPTIDE.
 FT DISULF 71 76 REMOVED IN MATURE FORM BY ENDOPEPTIDASE.
 FT MOD RES 106 106 AMIDATION (G-107 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 115 AA: 12438 MW: 453D11255CA53D1 CRC64;

Query Match 45.7%; Score 68.5; DB 1; Length 115;
 Best Local Similarity 53.3%; Pred. No. 0.0021;
 Matches 16; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

OY 1 HRLAGLSRSGGWKSNFVPTNVGSKAF 30
 DB 78 TORLADFLSRSGIGSPDF-VPTDVSANSF 106

RESULT 10
 IAPP_SAGEO STANDARD; PRT; 32 AA.
 AC Q28934;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Islet amyloid polypeptide (Amylin) (Fragment).

GN IAPP.
 OS Saginus oedipus (Cotton-top tamarin).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
 NCBI_TaxID=9490;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Albrandt K., Sierzega M.E., Mull E., Brady E.M.G.;
 RL Submitted (Aug-1996) to the EMBL/Genbank/DBP databases.
 CC -1- FUNCTION: SELECTIVELY INHIBITS INSULIN-STIMULATED GLUCOSE
 CC UTILIZATION AND GLYCOGEN DEPOSITION IN MUSCLE, WHILE NOT AFFECTING
 CC ADIPOCYTE GLUCOSE METABOLISM.
 CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
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 CC -----
 DR EMBL: U62627; AAB05918.1; -
 DR InterPro: IPR001693; Calc_CGRP_IAPP.
 DR Pfam: PF00214; Calc_CGRP_IAPP; 1.
 DR SMART: SM00113; CALCITONIN; 1.
 DR PROSITE: PS00258; CALCITONIN; PARTIAL.
 KW Hormone; Amyloid.
 FT NON-TER 1 1
 FT PEPTIDE <1 >32 ISLET AMYLOID POLYPEPTIDE.
 FT NON-TER 32 32
 SQ SEQUENCE 32 AA: 3340 MW: 91A219AE83882C02 CRC64;

Query Match 35.7%; Score 53.5; DB 1; Length 32;
 Best Local Similarity 51.7%; Pred. No. 0.1;
 Matches 15; Conservative 2; Mismatches 5; Indels 7; Gaps 2;

OY 2 HRLAGLSRSGGWKSNF--VPTNVGSK 27
 DB 8 HRLADFLGRS-----SNNFGALISPTNVGS 32

RESULT 11
 PA2D_MOUSE STANDARD; PRT; 144 AA.
 AC Q9WVF6; Q9JLK0;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Group IID secretory phospholipase A2 precursor (EC 3.1.1.4)
 DE (Phosphatidylcholine 2-acylhydrolase GIID) (GIID sPLA2) (PLA2IID)
 DE (sPLA(2)-IID) (Secretory-type PLA, stroma-associated homolog).
 GN PLA2G2D OR PLA2A2 OR SPLASH.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RC STRATN-BALB/C;
 RX MEDLINE=99386983; PubMed=10455175;
 RA Ishizaki T., Suzuki N., Higashino K.-I., Yokota Y., Ono T.,
 RA Kawamoto K., Fujii N., Arita H., Hanasaki K.;
 RT "Cloning and characterization of novel mouse and human secretory
 RT phospholipase A2s".
 RL J. Biol. Chem. 274:24973-24979(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=99315857; PubMed=10383420;
 RA Valentin E., Koduri R.S., Scimeca J.-C., Carle G., Gelb M.H.,
 RA Lazdunski M., Lambeau G.;
 RT "Cloning and recombinant expression of a novel mouse secreted

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DB PROSITE; PS00118; PA2_HIS; 1.
KW Hydroxylase; Lipid degradation; Signal; Calcium; Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 144
FT ACT_SITE 66 66 BY SIMILARITY.
FT ACT_SITE 111 111 BY SIMILARITY.
FT DISULFID 45 137 BY SIMILARITY.
FT DISULFID 47 63 BY SIMILARITY.
FT DISULFID 62 117 BY SIMILARITY.
FT DISULFID 68 144 BY SIMILARITY.
FT DISULFID 69 110 BY SIMILARITY.
FT DISULFID 78 103 BY SIMILARITY.
FT DISULFID 96 108 BY SIMILARITY.
FT CARBOHYD 99 99 N-LINKED (GLCNAC.. ) (POTENTIAL).
FT CA_BIND 46 46 VIA CARBONYL OXYGEN (BY SIMILARITY).
FT CA_BIND 48 48 VIA CARBONYL OXYGEN (BY SIMILARITY).
FT CA_BIND 50 50 VIA CARBONYL OXYGEN (BY SIMILARITY).
FT VASAPLIC 67 67 BY SIMILARITY..
FT VASAPLIC 1 26 MISSING (IN ISOFORM 2).
SQ SEQUENCE 144 AA; 16164 MW; 7697ADAD07F8D270A CRC64;

Query Match 34.7%; Score 52; DB 1; Length 144;
Best Local Similarity 40.7%; Pred. No. 0.83;
Matches 11; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

OY 4 LAGLISRSRGMYKSNFVPTNYSKAF 30
   |||: |||: | | | | | | |
DB 11 LAGITAFQCGILNKKNVTHMTGKKAFF 37

RESULT 12
IAPP_FELCA STANDARD: PRT; 89 AA.
AC P12967;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Islet amyloid polypeptide precursor (Amylin).
GN IAPP.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=89345542; PubMed=2668946;
RA Nishii M., Chan S.-J., Nagamatsu S., Bell G.I., Steiner D.F.;
RT "Conservation of the sequence of islet amyloid polypeptide in five
RT mammals is consistent with its putative role as an islet hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:5738-5742(1989).
RN [2]
RP SEQUENCE OF 34-50.
RP MEDLINE=87231921; PubMed=3035556;
RA Westermarck P., Wernstedt C., Wllander E., Hayden D.W., O'Brien T.D.,
RA Johnson K.H.;
RT "Amyloid fibrils in human insulinoma and islets of Langerhans of the
RT diabetic cat are derived from a neuropeptide-like protein also
RT present in normal islet cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:3881-3885(1987).
CC -!- FUNCTION: SELECTIVELY INHIBITS INSULIN-STIMULATED GLUCOSE
CC UTILIZATION AND GLYCOGEN DEPOSITION IN MUSCLE, WHILE NOT AFFECTING
CC ADIPOCYTE GLUCOSE METABOLISM.
CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
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DR EMBL; M25388; AAA30813.1; -
 DR PIR; A33542; A33542.
 DR PIR; B26619; B26619.
 DR InterPro; IPR001693; Calc_CGR_TAPP.
 DR InterPro; IPR000443; Islet_Amyloid.
 DR Pfam; PF00214; Calc_CGR_TAPP; 1.
 DR PRINTS; PR00818; ISLETAMYLOID.
 DR SMART; SM00113; CALCITONIN; 1.
 DR PROSITE; PS00258; CALCITONIN; 1.
 DR Hormone; Cleavage on pair of basic residues; Amidation; Amyloid;
 KW Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT PEPTIDE 34 70 ISLET AMYLOID POLYPEPTIDE.
 FT DISULFID 35 40 BY SIMILARITY.
 FT MOD_RES 70 70 AMIDATION (G-71 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 89 AA: 9831 MW: 0834D783DEAD72A8 CRC64;

Query Match 33.7%; Score 50.5; DB 1; Length 89;
 Best Local Similarity 43.3%; Pred. No. 0.85;
 Matches 13; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

Oy 1 THRLAGLLSRSGMKSNFYVPTNGSKAF 30
 Db 42 TORLANFLIRSSNNLGA-TLSPTNGSNFY 70

RESULT 13
 FMQ_MORBO STANDARD; PRT; 157 AA.
 AC P07640;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Fibrital protein Q precursor (Beta pilin) (Q pilin).
 GN TFPO.
 OS Moraxella bovis.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
 OX NCBI_TaxID=476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EPP63;
 RX MEDLINE=85234350; PubMed=2861194;
 RA Marrs C.F., Schoolnik G., Koomey J.M., Hardy J., Rothbard J.,
 RA Falkow S.;
 RT "Cloning and sequencing of a Moraxella bovis pilin gene";
 RL J. Bacteriol. 163:132-139(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EPP63;
 RX MEDLINE=90094235; PubMed=2403542;
 RA Fuiks K.A., Marrs C.F., Stevens S.P., Green M.R.;
 RT "Sequence analysis of the inversion region containing the pilin genes
 RT of Moraxella bovis";
 RL J. Bacteriol. 172:310-316(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=91286182; PubMed=2061282;
 RA Roza F.W., Marrs C.F.;
 RT "Interesting sequence differences between the pilin gene inversion
 RT regions of Moraxella lacunata ATCC 17956 and Moraxella bovis Epp63";
 RL J. Bacteriol. 173:4000-4006(1991).
 RN [4]
 RP SEQUENCE OF 7-157.
 RX MEDLINE=89010522; PubMed=2902184;
 RA Ruehl W.W., Marrs C.F., Fernandez R., Falkow S., Schoolnik G.K.;
 RT "Purification, characterization, and pathogenicity of Moraxella bovis
 RT pilli";
 RL J. Exp. Med. 168:983-1002(1988).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

CC -1- MISCELLANEOUS: MORAXELLA BOVIS CAN EXPRESS EITHER A Q OR A I
 CC PILIN, THE INVERSION OF 2 KB OF DNA DETERMINES WHICH PILIN IS
 CC EXPRESSED.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M11435; AAA25304.1; -
 DR EMBL; M32345; AAA88223.1; -
 DR EMBL; M59712; AAA825308.1; -
 DR PIR; A24434; A24434.
 DR PIR; J10072; J10072.
 DR InterPro; IPR001082; Pilin.
 DR InterPro; IPR001120; Prok_N_methyltn.
 DR Pfam; PF00114; pilin; 1.
 DR ProDom; PD000566; Pilin; 1.
 DR PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
 KW Fibrital; Methylation.
 FT PROPEP 1 6 FIBRITAL PROTEIN Q.
 FT CHAIN 7 157 METHYLATION.
 FT MOD_RES 7 7 BY SIMILARITY.
 FT DISULFID 136 155
 SQ SEQUENCE 157 AA: 16006 MW: A923CD8A26C693C9 CRC64;

Query Match 32.7%; Score 49; DB 1; Length 157;
 Best Local Similarity 39.1%; Pred. No. 2.6;
 Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Oy 8 LSRSGMKSNFYVPTNGSKAF 30
 Db 78 LTTTGCTARSNLMSVNIIGGAF 100

RESULT 14
 GUX1_PHACH STANDARD; PRT; 516 AA.
 ID GUX1_PHACH
 AC P13860;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Exoglucanase I precursor (EC 3.2.1.91) (Exocellulohydrolase I)
 DE (1,4-beta-cellobiohydrolase).
 GN CBHL.
 OS Phanerochaete chrysosporium.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Corticiaceae; Phanerochaete.
 OX NCBI_TaxID=5306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ME446;
 RX MEDLINE=89232732; PubMed=3246351;
 RA Sims P.F.G., James C., Broda P.;
 RT "The identification, molecular cloning and characterisation of a gene
 RT from Phanerochaete chrysosporium that shows strong homology to the
 RT exo-cellobiohydrolase I gene from Trichoderma reesei";
 RL Gene 74:411-422(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ME446;
 RX MEDLINE=94335641; PubMed=8057846;
 RA Sims P.F.G., Soares-Felipe M.S., Wang Q., Gent M.E., Tempelaars C.,
 RA Broda P.;
 RT "Differential expression of multiple exo-cellobiohydrolase I-like
 RT genes in the lignin-degrading fungus Phanerochaete chrysosporium";
 RL Mol. Microbiol. 12:209-216(1994).
 CC -1- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE

```

CC CC      GENERALY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:
CC CC      (1) EXOGLUCANASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;
CC CC      (2) EXOCELLULOBIOTIC HYDROLASES THAT CUT THE DISSACCHARIDE CELLULOSE
CC CC      FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;
CC CC      (3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLULOSE AND OTHER
CC CC      SHORT BETA-1,4-GLUCOSACCHARIDES TO GLUCOSE.
CC CC      -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
CC CC      in cellulose and cellotetraose, releasing cellobiose from the non-
CC CC      reducing ends of the chains.
CC CC      -1- SUBCELLULAR LOCATION: Secreted.
CC CC      -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY C (FAMILY 7 OF GLYCOSYL
CC CC      HYDROLASES).
CC CC      -1- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBR).
CC CC      -----
CC CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC CC      use by non-profit institutions as long as its content is in no way
CC CC      modified and this statement is not removed. Usage by and for commercial
CC CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC      or send an email to license@isb-sib.ch).
CC CC      -----
DR EMBL: M22220; AAB46373.1; -
DR EMBL: M22228; CAB80253.1; -
DR PIR: JS0083; JS0083.
DR HSSP: P00725; 2CBH.
DR InterPro: IPR000254; Glyco_hydro_7.
DR InterPro: IPR001722; Glyco_hydro_7.
DR Pfam: PF00734; CBD_1; 1.
DR Pfam: PF00840; Glyco_hydro_7; 1.
DR PRINTS: PR00734; GLHYDRLASE7.
DR ProDom: PD001821; CBD_fungal; 1.
DR ProDom: PD186135; Glyco_hydro_7; 1.
DR SMART: SM00236; fcbd; 1.
DR PROSITE: PS00562; CBD_FUNGAL; 1.
DR Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
KW SIGNAL
FT SIGNAL 1 18
FT CHAIN 19 516
FT DOMAIN ? 449
FT DOMAIN ? 449
FT DOMAIN 450 480
FT DOMAIN 481 516
FT ACT_SITE 225 225
FT ACT_SITE 230 230
FT CARBOHYD 208 208
FT CARBOHYD 326 326
FT CARBOHYD 442 442
FT DISULFID 488 505
FT DISULFID 499 515
FT DISULFID 27 28
FT CONFLICT 30 31
FT CONFLICT 31
SQ SEQUENCE 516 AA; 54857 MW; 1C7C3D338ECE1B72 CRC64;

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Query Match 32.7%; Score 49; DB 1; Length 516;
Best Local Similarity 39.1%; Pred. No. 8.9;
Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
Oy 8 LRSRSGMVKNSFVPTNGSKAF 30
Db 102 ITASGSSLKLPFTGNSVNGSRV 124

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RESULT 15
IAPP_MOUSE STANDARD; PRT; 93 AA.
AC P12968:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Islet amyloid polypeptide precursor (Diabetes-associated peptide)
DE (DAP) (Amylin).
GN IAPP.
OS Mus musculus (Mouse).

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OC CC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC CC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC CC      NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89345542; PubMed=2668946;
RA Nishi M., Chan S.J., Nagamatsu S., Bell G.I., Steiner D.F.;
RT "Conservation of the sequence of islet amyloid polypeptide in five
RT mammals is consistent with its putative role as an islet hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:5738-5742(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2J; TISSUE=Liver;
RX MEDLINE=97424750; PubMed=9278863;
RA Ekawa K., Nishi M., Ohagi S., Sanke T., Nanjo K.;
RT "Cloning of mouse islet amyloid polypeptide gene and characterization
RT of its promoter.";
RL J. Mol. Endocrinol. 19:79-86(1997).
RN [3]
RP SEQUENCE OF 38-74.
RX MEDLINE=89325677; PubMed=2666169;
RA Betsholtz C., Christmansson L., Engstrom U., Rorsman F., Svensson V.,
RA Johnson K.H., Westermark P.;
RT "Sequence divergence in a specific region of islet amyloid
RT polypeptide (IAPP) explains differences in islet amyloid formation
RT between species.";
RL FEBS Lett. 251:261-264(1989).
CC -1- FUNCTION: SELECTIVELY INHIBITS INSULIN-STIMULATED GLUCOSE
CC UTILIZATION AND GLYCOGEN DEPOSITION IN MUSCLE, WHILE NOT AFFECTING
CC ADIPOCYTE GLUCOSE METABOLISM.
CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
CC CC      -----
CC CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC CC      use by non-profit institutions as long as its content is in no way
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CC CC      or send an email to license@isb-sib.ch).
CC CC      -----
DR EMBL: M25369; AAA37874.1; -
DR EMBL: D31820; BAA22051.1; -
DR EMBL: D31819; BAA22051.1; JOINED.
DR PIR: S05039; S05039.
DR PIR: C33542; C33542.
DR MGD: MG1:96382; IAPP.
DR InterPro: IPR001693; Calc_CGRP_IAPP.
DR InterPro: IPR000443; Calc_CGRP_IAPP.
DR Pfam: PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS: PR00818; ISLETAMYLID.
DR SMART: SM00113; CALCITONIN; 1.
DR PROSITE: PS00258; CALCITONIN; 1.
KW Hormone; Cleavage on pair of basic residues; Amidation; Amyloid;
KW SIGNAL.
FT SIGNAL 1 23
FT PEPTIDE 38 74
FT DISULFID 39 74
FT MOD_RES 74 74
SQ SEQUENCE 93 AA; 10022 MW; B135DBC81475B15 CRC64;

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Query Match 32.3%; Score 48.5; DB 1; Length 93;
Best Local Similarity 43.3%; Pred. No. 1.8;
Matches 13; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

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Oy 1 THRLAGLRSRSGMVKNSFVPTNGSKAF 30
Db 46 TÖRLANFLVRSSNNL-GVPLPTNGSNTY 74

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Search completed: August 26, 2002, 15:53:25
Job time: 121 sec

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10/10/2002 10:02:51 AM

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 26, 2002, 15:49:48 ; Search time 12.97 Seconds
(without alignments)
56.497 Million cell updates/sec

Title: US-09-813-345-2
Perfect score: 150
Sequence: 1 THRAGILSRSGMWKSNFVPTVNGSKAF 30

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	150	100.0	30	4	US-09-070-504-2
2	135.5	90.3	29	4	US-09-070-504-1
3	135.5	90.3	37	1	US-08-233-389C-9
4	135.5	90.3	37	2	US-08-801-863-9
5	135.5	90.3	37	2	US-08-486-596A-9
6	135.5	90.3	37	2	US-09-004-713-9
7	135.5	90.3	37	2	US-08-619-841-2
8	135.5	90.3	37	2	US-08-446-929A-2
9	135.5	90.3	37	4	US-09-070-504-3
10	135.5	90.3	38	1	US-07-776-272-20
11	131.5	87.7	37	4	US-09-070-504-8
12	128.5	85.7	29	1	US-07-794-288D-26
13	128.5	85.7	30	1	US-07-794-288D-27
14	128.5	85.7	35	2	US-08-460-890A-45
15	128.5	85.7	35	3	US-08-167-641C-45
16	128.5	85.7	35	4	US-08-462-040-45
17	128.5	85.7	35	4	US-08-462-040-45
18	128.5	85.7	37	1	US-07-794-288D-3
19	128.5	85.7	37	1	US-08-233-389C-8
20	128.5	85.7	37	2	US-08-801-863-8
21	128.5	85.7	37	2	US-08-486-596A-8
22	128.5	85.7	37	2	US-09-004-713-8
23	128.5	85.7	37	2	US-08-619-841-1
24	128.5	85.7	37	2	US-08-446-929A-1
25	128.5	85.7	37	4	US-09-070-504-4
26	128.5	85.7	37	6	US-07-794-288D-96
27	128.5	85.7	38	1	US-07-776-272-19

28	128.5	85.7	38	2	US-08-460-890A-44	Sequence 44, Appl
29	128.5	85.7	38	3	US-08-167-641C-44	Sequence 44, Appl
30	128.5	85.7	38	4	US-08-460-971A-44	Sequence 44, Appl
31	128.5	85.7	38	4	US-08-462-040-44	Sequence 44, Appl
32	127.5	85.0	37	4	US-09-070-504-5	Sequence 5, Appl
33	127.5	85.0	37	4	US-09-070-504-10	Sequence 10, Appl
34	127.5	85.0	37	4	US-09-070-504-11	Sequence 11, Appl
35	127.5	85.0	38	1	US-07-794-288D-127	Sequence 127, App
36	126.5	84.3	37	4	US-09-070-504-9	Sequence 9, Appl
37	123.5	82.3	28	1	US-07-794-288D-28	Sequence 28, Appl
38	123.5	82.3	37	4	US-09-070-504-6	Sequence 6, Appl
39	123.5	82.3	38	1	US-07-776-272-21	Sequence 21, Appl
40	123.5	81.7	28	1	US-07-794-288D-127	Sequence 127, App
41	121.5	81.7	29	1	US-07-794-288D-72	Sequence 72, Appl
42	121.5	81.0	37	6	5424221-5	Patent No. 5424221
43	121	80.7	29	1	US-07-794-288D-96	Sequence 96, App
44	118.5	79.0	27	1	US-07-794-288D-128	Sequence 128, App
45	118.5	79.0	28	1	US-07-794-288D-73	Sequence 73, Appl

ALIGNMENTS

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RESULT 1
US-09-070-504-2
; Sequence 2, Application US/09070504
; Patent No. 6268474
GENERAL INFORMATION:
APPLICANT: Smith, Derek D.
APPLICANT: Sana, Shankar
APPLICANT: Abel, Peter W.
TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: Metling, Raasch & Gebhardt, P. A.
STREET: 119 No. 6268474th Fourth Street
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,504
FILING DATE: 30-Apr-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McCormick, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180,00020101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-070-504-2

Query Match 100.0%; Score 150; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 THRAGILSRSGMWKSNFVPTVNGSKAF 30
|||||
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DB 1 THRLAGLSRSGMVKSNFVPTNVGSKAF 30

RESULT 2

US-09-070-504-1

Sequence 1, Application US/09070504

Patent No. 6268474

GENERAL INFORMATION:

APPLICANT: Smith, Derek D.

APPLICANT: Saha, Shankar

APPLICANT: Abel, Peter W.

TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR

TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mueling, Raasch & Gebhardt, P.A.

STREET: 119 No. 6268474th Fourth Street

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/070,504

FILING DATE: 30-APR-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: McCormack, Myra H

REGISTRATION NUMBER: 36,602

REFERENCE/DOCKET NUMBER: 180.00020101

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612/305-1220

TELEFAX: 612/305-1228

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-070-504-1

Query Match 90.3%; Score 135.5; DB 4; Length 29;

Best Local Similarity 96.7%; Pred. No. 1.3e-13;

Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 THRLAGLSRSGMVKSNFVPTNVGSKAF 30

DB 1 THRLAGLSRSGMVKSNFVPTNVGSKAF 29

RESULT 3

US-08-233-389C-9

Sequence 9, Application US/08233389C

Patent No. 5639855

GENERAL INFORMATION:

APPLICANT: KITAMURA, Kazuo

APPLICANT: KANGAWA, Kenji

APPLICANT: MATSUO, Hisayuki

APPLICANT: ETO, Tanenao

TITLE OF INVENTION: ADRENOMEDULLIN

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: C/O FISH & NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/233,389C

FILING DATE: 26-APR-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: HALEY JR., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: SHGN-5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-233-389C-9

Query Match 90.3%; Score 135.5; DB 1; Length 37;

Best Local Similarity 96.7%; Pred. No. 1.7e-13;

Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 THRLAGLSRSGMVKSNFVPTNVGSKAF 30

DB 9 THRLAGLSRSGMVKSNFVPTNVGSKAF 37

RESULT 4

US-08-801-863-9

Sequence 9, Application US/08801863

Patent No. 5830703

GENERAL INFORMATION:

APPLICANT: KITAMURA, Kazuo

APPLICANT: KANGAWA, Kenji

APPLICANT: MATSUO, Hisayuki

APPLICANT: ETO, Tanenao

TITLE OF INVENTION: ADRENOMEDULLIN

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: C/O FISH & NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/801,863

FILING DATE: CONCURRENTLY HERewith

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: HALEY JR., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: SHGN-5 DIV3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

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;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-801-863-9

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Query Match	90.38;	Score 135.5;	DB 2;	Length 37;
Best Local Similarity	96.78;	Pred. No. 1.7e-13;		
Matches 29;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1

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OY      1 THRLAGLLSRGGMVKSNEVPTNVGSKAF    30  
          |||||  
Db       9 THRLAGLLSRGGMVKSNE-VPTNVGSKAF   37
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RESULT 5
US-08-486-596A-9
; Sequence 9, Application US/08486596A
; Patent No. 5937893

APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUDO, Hisayuki
APPLICANT: ETO, Taneao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY

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1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: Parental Release #1.0, Version #1.33
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/08/486,596A
8  FILING DATE: JUNE 7, 1995
9  CLASSIFICATION: 530

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; SEQUENCE CHARACTERISTICS
; LENGTH: 37 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-486-596A-9

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Query Match %	90.3%	Score 135.5	DB 2	Length 37
Best Local Similarity	96.7%	Pred. No. 1.7e-13		
Matches 29	Conservative 0	Mismatches 0	Indels 1	Gaps 1

Qy	1	THRLAGLLSRSGGMVKS	NFVPTNVGSKAF	30
Db	9	THRLAGLLSRSGGMVKS	NFVPTNVGSKAF	37

RESULT 6
US-09-004-713-9
; Sequence 9, Application US/09004713-9
; Patent No. 5910416
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji

1 APPLICANT: MATSUO, Hisayuki
2
3 APPLICANT: ETO, Tanenao
4
5 TITLE OF INVENTION: ADRENOMEDULLIN
6
7 NUMBER OF SEQUENCES: 10
8
9 CORRESPONDENCE ADDRESS:
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ADDRESS: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10020

COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM
MEDTUM ENDR. E]COM

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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: Patent In Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; ADDITION NUMBER: 05/06/2004 713

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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids

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;      MOLECULE TYPE:      protein
US-09-004-713-9

Query Match      90.3%      Score 135.5; DB 2; Length 37;
Best Local Similarity 96.7%; Pred.No. 1.7e-13;
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1.

QY      1  THRAGLLSRSGCMWKSNFVPTNGSKAF 30

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Db 9 THRAGLTSRRCGKVNKNF-VPTNYSKAF 37

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1 GENERAL INFORMATION:
2
3 APPLICANT: Vallampally, Chandrasekhar
4
5 APPLICANT: Wimalawansa, Sunil J.
6
7 TITLE OF INVENTION: Treatment or Prevention of Preeclampsia,
8
9 TITLE OF INVENTION: Eclampsia, or Preeclam Labor with Calciumin Gene Related
10
11 TITLE OF INVENTION: Peptide, CGRP Analog, Progestational Agent, Nitric Oxide

```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P. O. Box 4433
;;

STATE: TX
COUNTRY: USA
ZIP: 77210-4433

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ATTORNEY/AGENT INFORMATION:
NAME: Hoddins, Daniel S.
REGISTRATION NUMBER: 31,026
REFERENCE/DOCKET NUMBER: UTSG:195\HOD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-619-841-2

Query Match 90.3%; Score 135.5; DB 2; Length 37;
Best Local Similarity 96.7%; Pred. No. 1.7e-13;
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 THRAGLLSRSGMVKSNFVPTNVGSKAF 30
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Db 9 THRAGLLSRSGMVKSNF-VPTNVGSKAF 37

RESULT 8
US-08-446-929A-2
Sequence 2, Application US/08446929A
Patent No. 5958877
GENERAL INFORMATION:
APPLICANT: Wimalawansa, Sunil J.
TITLE OF INVENTION: A Method for Counteracting
TITLE OF INVENTION: Vasospasms, Ischemia, Renal Failure, and Treating Male
TITLE OF INVENTION: Impotence Using Calcitonin Gene Related Peptide
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rosenblatt & Redano, P.C.
STREET: One Greenway Plaza, Suite 500
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77046-0103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.0 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5.3
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,929A
FILING DATE: 18-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Mossman, David L.
REGISTRATION NUMBER: 29,570
REFERENCE/DOCKET NUMBER: LEOC-90
TELECOMMUNICATION INFORMATION:
TELEPHONE: 210/542-8339
TELEFAX: 210/544-7201
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: n/a
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE:
PUBLICATION INFORMATION:
AUTHORS: Wimalawansa, Sunil J.
TITLE: Calcitonin: Molecular Biology, Physiology,
Title: Pathophysiology and Its Therapeutic Uses

JOURNAL: Advances in Bone Regulatory Factors
JOURNAL: Morphology, Biochemistry, Physiology and Pharmacology
JOURNAL:
VOLUME: n/a
ISSUE: n/a
PAGES: 121-160
DATE: 1989
US-08-446-929A-2

Query Match 90.3%; Score 135.5; DB 2; Length 37;
Best Local Similarity 96.7%; Pred. No. 1.7e-13;
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 THRAGLLSRSGMVKSNFVPTNVGSKAF 30
|||||
Db 9 THRAGLLSRSGMVKSNF-VPTNVGSKAF 37

RESULT 9
US-09-070-504-3
Sequence 3, Application US/09070504
Patent No. 6268474
GENERAL INFORMATION:
APPLICANT: Smith, Derek D.
APPLICANT: Saha, Shankar
APPLICANT: Abel, Peter W.
TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueitng, Raasch & Gebhardt, P.A.
STREET: 119 No. 6268474th Fourth Street
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,504
FILING DATE: 30-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-070-504-3

Query Match 90.3%; Score 135.5; DB 4; Length 37;
Best Local Similarity 96.7%; Pred. No. 1.7e-13;
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 THRAGLLSRSGMVKSNFVPTNVGSKAF 30
|||||
Db 9 THRAGLLSRSGMVKSNF-VPTNVGSKAF 37

RESULT 10

US-07-776-272-20
; Sequence 20, Application US/07776272
; Patent No. 5612454
; GENERAL INFORMATION:
; APPLICANT: Kaminuma, Toshihiko
; APPLICANT: Iida, Toshi
; APPLICANT: Tajima, Masahito
; TITLE OF INVENTION: Process for Purification of Polypeptide
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wegner, Cantor, Mueller & Player
; STREET: 1233 20th St. N.W. P.O. Box 18218
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: United States of America
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/776,272
; FILING DATE: 19911129
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P-450-23167
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-0400
; TELEFAX: 202-887-0605
; TELEX: 440706
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Human
; US-07-776-272-20

Query Match 90.3%; Score 135.5; DB 1; Length 38;
Best Local Similarity 96.7%; Pred. No. 1.8e-13;
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGWKSNFVPTNVGSKAF 30
Db 9 THRLAGLSRSGGWKSNF-VPTNVGSKAF 37

RESULT 11
US-09-070-504-8
; Sequence 8, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; APPLICANT: Saha, Shankar
; APPLICANT: Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueling, Raasch & Gebhardt, P. A.
; STREET: 119 No. 6268474th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,504
; FILING DATE: 30-Apr-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180,00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-070-504-8

Query Match 87.7%; Score 131.5; DB 4; Length 37;
Best Local Similarity 93.3%; Pred. No. 6.8e-13;
Matches 28; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGWKSNFVPTNVGSKAF 30
Db 9 THRLAGLSRSGGWKSNF-VPTNVGSEAF 37

RESULT 12
US-07-794-288D-27
; Sequence 27, Application US/07794288D
; Patent No. 5580953
; GENERAL INFORMATION:
; APPLICANT: ELISABETH ALBRECHT,
; APPLICANT: HOWARD JONES,
; APPLICANT: LAURA S.L. GAETA,
; APPLICANT: KATHRYN S. PRICKETT and
; APPLICANT: KEVIN BEAUMONT
; TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: First Interstate World
; STREET: Center
; STREET: 633 West Fifth Street,
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44
; MEDIUM TYPE: 5.25" Diskette, 1.44
; MEDIUM TYPE: 5.25" Diskette, 1.44
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: IBM M.S. DOS (Version
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/794,288D
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/794,288
; FILING DATE: 19-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Duff, Bradford, J.

REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 193/153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
FEATURE:
OTHER INFORMATION:
US-07-794-288D-27

Query Match 85.7%; Score 128.5; DB 1; Length 29;
Best Local Similarity 90.0%; Pred. No. 1.4e-12;
Matches 27; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 1 THRLAGLSRSGGVKNNF-VPTNVGSKAF 30
Db 1 THRLAGLSRSGGVKNNF-VPTNVGSKAF 29

RESULT 13
US-07-794-288D-26
Sequence 26, Application US/07794288D
Patent No. 5580953
GENERAL INFORMATION:
APPLICANT: ELISABETH ALBRECHT,
APPLICANT: HOWARD JONES,
APPLICANT: LAURA S.L. GAETA,
APPLICANT: KATHRYN S. PRICKETT and
APPLICANT: KEVIN BEADMON
TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST
TITLE OF INVENTION: PEPTIDES AND USES THEREFOR
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: First Interstate World
STREET: Center
STREET: 633 West Fifth Street,
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
MEDIUM TYPE: Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: IBM M.S. DOS (Version
5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/794,288D
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/794,288
FILING DATE: 19-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Duft, Bradford, J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 193/153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:

LENGTH: 30 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
FEATURE:
OTHER INFORMATION:
US-07-794-288D-26

Query Match 85.7%; Score 128.5; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 1.5e-12;
Matches 27; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 1 THRLAGLSRSGGVKNNF-VPTNVGSKAF 30
Db 2 THRLAGLSRSGGVKNNF-VPTNVGSKAF 30

RESULT 14
US-08-460-890A-45
Sequence 45, Application US/08460890A
Patent No. 5994109
GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,890A
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: "Xaa" stands for an unnatural amino
acid with R group forming a ring
OTHER INFORMATION: acid with R group forming a ring

OTHER INFORMATION: attached to "Asp" in position 1.
OTHER INFORMATION: "Lys" in position 22 has an
OTHER INFORMATION: n-x substitution.
US-08-460-890A-45

Query Match 85.7%; Score 128.5; DB 2; Length 35;
Best Local Similarity 90.0%; Pred. No. 1.8e-12;
Matches 27; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGVKSNFVPTNGSKAF 30
Db 7 THRLAGLSRSGGVKSNF-VPTNGSKAF 35

RESULT 15
US-08-167-641C-45

Sequence 45; Application US/08167641C
Patent No. 6033884

GENERAL INFORMATION:

APPLICANT: Woo, Savio L.C.

APPLICANT: Smith, Louis C.

APPLICANT: Cristiano, Richard J.

APPLICANT: Gottchalk, Stephen

TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND

TITLE OF INVENTION: METHODS OF USE

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/167,641C

FILING DATE: December 14, 1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/855,389

FILING DATE: March 20, 1992

APPLICATION NUMBER: PCT/US93/02725

FILING DATE: March 19, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 205/012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

OTHER INFORMATION: "Xaa" stands for an unnatural amino

OTHER INFORMATION: acid with R group forming a ring

OTHER INFORMATION: attached to "Asp" in position 1.

OTHER INFORMATION: "Lys" in position 22 has an

OTHER INFORMATION: n-x substitution.

Query Match 85.7%; Score 128.5; DB 3; Length 35;
Best Local Similarity 90.0%; Pred. No. 1.8e-12;
Matches 27; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGVKSNFVPTNGSKAF 30
Db 7 THRLAGLSRSGGVKSNF-VPTNGSKAF 35

Search completed: August 26, 2002, 15:52:15
Job time: 147 sec

